GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 11:55:42 ; Search time 5327 Seconds
(without alignments)
10740.155 Million cell updates/sec

Title: US-09-430-775-1
Perfect score: 1320
Sequence: 1 AGTATTGTTTGTCTGTTTGC.....CCAGCATTCCTGGCTTTCTG 1320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1320	100.0	1320	6	AR075909	AR075909 Sequence
2	1320	100.0	1320	6	AR083195	AR083195 Sequence
3	1320	100.0	1320	6	I20778	I20778 Sequence 1
4	1304.8	98.8	75031	9	AL390716	AL390716 Human DNA
5	1300	98.5	1452	9	HSPP1GN	Z66526 H.sapiens p
6	1283.6	97.2	1673	9	HSU42387	U42387 Human pancr
7	1210	91.7	53269	2	AC006184	AC006184 Homo sapi
8	1180	89.4	1180	6	AR270498	AR270498 Sequence
9	1180	89.4	1180	9	HSU35232	U35232 Human neuro
10	1128	85.5	1128	6	AX548917	AX548917 Sequence
11	1120	84.8	1128	9	AY268432	AY268432 Homo sapi
12	1051.2	79.6	1128	9	AY149475	AY149475 Macaca mu
13	982.6	74.4	1796	4	AB021678	AB021678 Sus scrof
14	896.6	67.9	1128	4	AF227955	AF227955 Sus scrof
15	828.6	62.8	1119	10	AF072822	AF072822 Cavia por
c 16	811.2	61.5	224691	2	AC129870	AC129870 Rattus no
c 17	811.2	61.5	249291	2	AC109718	AC109718 Rattus no
18	810.8	61.4	1439	6	AR083220	AR083220 Sequence
19	807.8	61.2	1500	6	AX418272	AX418272 Sequence
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23	780.6	59.1	1209	10	RNPP1GN	Z68180 R.norvegicu
24	762.2	57.7	1128	10	RNU84245	U84245 Rattus norv
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27	364	27.6	1098	5	AF340022	AF340022 Lampetra
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31	303	23.0	1846	10	BC051420	BC051420 Mus muscu
32	303	23.0	2157	10	MUSNYY1RA	D63818 Mouse mRNA
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42	266	20.2	1499	6	I40470	I40470 Sequence 11
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44	261.8	19.8	1299	4	D86521	D86521 Rabbit mRNA
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ALIGNMENTS

RESULT 1
AR075909
LOCUS AR075909 1320 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 1 from patent US 5958709.
ACCESSION AR075909
VERSION AR075909.1 GI:10002655
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1320)
AUTHORS Bard,J.A., Walker,M.W., Branchek,T. and Weinshank,R.L.
TITLE Processes for identifying compounds that bind to the human Y4 receptor
JOURNAL Patent: US 5958709-A 1 28-SEP-1999;

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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.7e-227;
  Matches 1320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
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Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
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Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
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RESULT 2
AR083195
LOCUS       AR083195                1320 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 1 from patent US 5976814.
ACCESSION   AR083195
VERSION     AR083195.1  GI:10009985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1320)
  AUTHORS   Bard,J.A., Walker,M.W., Branchek,T. and Weinshank,R.L.
  TITLE     DNA encoding a human neuropeptide Y/peptide YY/pancreatic
            polypeptide receptor (Y4) and uses thereof
  JOURNAL   Patent: US 5976814-A 1 02-NOV-1999;
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  Query Match             100.0%;  Score 1320;  DB 6;  Length 1320;
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LOCUS       I20778                 1320 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5516653.
ACCESSION   I20778
VERSION     I20778.1  GI:1601133
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1320)
  AUTHORS   Bard,J.A., Walker,M.W., Branchek,T. and Weinshank,R.L.
  TITLE     DNA encoding a human neuropeptide Y/peptide YY/pancreatic
            polypeptide receptor (Y4) and uses thereof
  JOURNAL   Patent: US 5516653-A 1 14-MAY-1996;
FEATURES             Location/Qualifiers
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  Matches 1320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
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Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200

Db       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200

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Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320

Db       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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RESULT 4
AL390716
LOCUS AL390716 75031 bp DNA linear PRI 16-AUG-2001
DEFINITION Human DNA sequence from clone RP11-314P12 on chromosome 10, complete sequence.
ACCESSION AL390716
VERSION AL390716.27 GI:15209414
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 75031)
AUTHORS Garner,P.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Aug 18, 2001 this sequence version replaced gi:14669300.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RP11-314P12 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-314P12 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-314P12 is at 1 in this sequence.
The true left end of clone RP11-144G6 is at 73032 in this sequence.
FEATURES Location/Qualifiers
source 1. .75031
/organism="Homo sapiens"
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/clone="RP11-314P12"
/clone_lib="RPCI-11.2"
misc_feature 35617. .35678
/note="Sequence from uni-directional dGTP big dye terminator reads only."
ORIGIN

Query Match 98.8%; Score 1304.8; DB 9; Length 75031;
Best Local Similarity 99.8%; Pred. No. 7.6e-225;
Matches 1317; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60

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Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120

Db      19452 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 19511

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180

Db      19512 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 19571

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240

Db      19572 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 19631

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300

Db      19632 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 19691

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Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420

Db      19752 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 19811

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480

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Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540

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Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600

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Db      19992 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 20051
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Db      20112 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 20171

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
Db      20172 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 20231

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
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Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
Db      20352 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 20411

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
Db      20412 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 20471

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
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Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
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Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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LOCUS       HSPP1GN                 1452 bp    DNA     linear   PRI 29-FEB-1996
DEFINITION  H.sapiens pancreatic polypeptide receptor PP1 gene.
ACCESSION   Z66526
VERSION     Z66526.1  GI:1107699
KEYWORDS    pancreatic polypeptide receptor; PP1 receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1452)
  AUTHORS   Lundell,I., Blomqvist,A.G., Berglund,M.M., Schober,D.A.,
            Johnson,D., Statnick,M.A., Gadski,R.A., Gehlert,D.R. and
            Larhammar,D.
  TITLE     Cloning of a human receptor of the NPY receptor family with high
            affinity for pancreatic polypeptide and peptide YY
  JOURNAL   J. Biol. Chem. 270 (49), 29123-29128 (1995)
  MEDLINE   96094298
   PUBMED   7493937
REFERENCE   2  (bases 1 to 1452)
  AUTHORS   Larhammar,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-1995) Dan Larhammar, Medical Pharmacology,
            Uppsala University, Uppsala, S-751 24, Sweden
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 98.5%; Score 1300; DB 9; Length 1452;
Best Local Similarity 99.5%; Pred. No. 1e-223;
Matches 1314; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
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Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
Db        120 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 179

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Db        180 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 239

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Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
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Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
Db        480 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 539

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
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Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
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Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
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Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
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Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
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Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
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Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
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Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
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Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
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Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
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Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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Db       1320 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1379
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RESULT 6
HSU42387
LOCUS HSU42387 1673 bp mRNA linear PRI 11-SEP-1996
DEFINITION Human pancreatic polypeptide receptor mRNA, complete cds.
ACCESSION U42387
VERSION U42387.1 GI:1314327
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1673)
AUTHORS Yan,H., Yang,J., Marasco,J., Yamaguchi,K., Brenner,S., Collins,F. and Karbon,W.
TITLE Cloning and functional expression of cDNAs encoding human and rat pancreatic polypeptide receptors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4661-4665 (1996)
MEDLINE 96209788
PUBMED 8643460
REFERENCE 2 (bases 1 to 1673)
AUTHORS Yan,H., Yang,J., Marasco,J., Yamaguchi,K., Brenner,S., Collins,F. and Karbon,W.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-1995) Hai Yan, Neuroscience, Amgen Inc., 1840 DeHavilland Drive, Thousand Oaks, CA 91362, USA
FEATURES Location/Qualifiers
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CDS 86. .1213
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ORIGIN

Query Match 97.2%; Score 1283.6; DB 9; Length 1673;
Best Local Similarity 99.3%; Pred. No. 9e-221;
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Qy         83 CCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAA 142
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Qy        203 ACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTA 262
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Db        201 ACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTA 260

Qy        263 ACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGC 322
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Qy        323 TTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCG 382
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Qy        383 CCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCT 442
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Qy        443 TCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGA 502
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Db        441 TCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGA 500

Qy        503 GGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGG 562
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Db        621 TCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCGGATAAGG 680

Qy        683 TGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGC 742
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Db        681 TGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGC 740

Qy        743 TCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACC 802
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Db        741 TCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCTTGGTCTGTTATGCACGCATCTACC 800

Qy        803 GGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGC 862
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Qy        923 TGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCC 982
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Qy        983 ACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACC 1042
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Qy       1043 CATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGA 1102
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Qy       1103 CTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATA 1162
Db       1101 CTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCAGAGCATCTGCCCCTGTCCACAGTACATA 1160

Qy       1163 CGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAACCAGGTC 1222
Db       1161 CGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAACCAGGTC 1220

Qy       1223 TAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTAGCTAAGTGGGCACACT 1282
Db       1221 TAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTAGCTAAGTGGGCACACT 1280

Qy       1283 GCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
Db       1281 GCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1318
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RESULT 7
AC006184
LOCUS       AC006184               53269 bp    DNA     linear   HTG 30-AUG-2001
DEFINITION  Homo sapiens chromosome 10 clone CRI-JC2032 map 10q11.2, 2 ordered
            pieces.
ACCESSION   AC006184
VERSION     AC006184.1  GI:3983513
KEYWORDS    HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 53269)
  AUTHORS   Smith,D.R.
  TITLE     Sequencing of Human Chromosome 10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 53269)
  AUTHORS   Smith,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-DEC-1998) Genome Therapeutics Corporation, 100 Beaver
            Street, Waltham, MA 02154, USA
COMMENT     Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing
            Technology. Data may contain low quality seq uence and BAC/Cosmid
            vector sequences.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1    30092: contig of 30092 bp in length
            *                   gap of unknown length
            *   30093    53269: contig of 23177 bp in length.
FEATURES             Location/Qualifiers
     source          1. .53269
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q11.2"
                     /clone="CRI-JC2032"
ORIGIN
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Query Match 91.7%; Score 1210; DB 2; Length 53269;
Best Local Similarity 96.9%; Pred. No. 8.7e-208;
Matches 1279; Conservative 0; Mismatches 34; Indels 7; Gaps 5;

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Qy           1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
Db        3359 AGTATTGTTTGTCTGTTGCCTTGTA-GGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 3417

Qy          61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
Db        3418 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 3477

Qy         121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
Db        3478 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 3537

Qy         181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
Db        3538 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 3597

Qy         241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
Db        3598 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 3657

Qy         301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
Db        3658 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTNN 3717

Qy         361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
Db        3718 CTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 3777

Qy         421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
Db        3778 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 3837

Qy         481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
Db        3838 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 3897

Qy         541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
Db        3898 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 3957

Qy         601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
Db        3958 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 4017

Qy         661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
Db        4018 CTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNTCACCACCGC 4077

Qy         721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
Db        4078 ACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGNTTCATNTTG 4137

Qy         781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
Db        4138 GTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 4197

Qy         841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
Db        4198 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 4257

Qy         901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
Db        4258 GTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 4317
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Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       4318 CATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 4377

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
              |||||||||||||| |||||||||||||||||||||||||| ||||||||||||||| ||
Db       4378 ATGGCCTCCACCTGTGTCAACCCATTCATCTATGGCTTTCT-AACACCAACTTCAAG-AG 4435

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
              ||||  ||||||||||||||||||||||||      | ||||||||||||||  ||||||
Db       4436 GAGAATAAGGCCCTGGTGCTGACTTGCCAG--AGAGGGCCCCCTGGAGGAGTAAGAGCAT 4493

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4494 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 4553

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db       4554 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGGTTTTC 4613

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
              |||||||||||||||||||||||||||||||||||||||||    |||||||||||||||
Db       4614 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCC--AGATTCCTGGCTTTCTG 4671
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RESULT 8
AR270498

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LOCUS       AR270498                1180 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1061 from patent US 6500938.
ACCESSION   AR270498
VERSION     AR270498.1  GI:29701732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1180)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE     Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1061 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1..1180
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             89.4%;  Score 1180;  DB 6;  Length 1180;
  Best Local Similarity   100.0%;  Pred. No. 4e-202;
  Matches 1180;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 60

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 120

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 180

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 240

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 300

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 360

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 420

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
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Db        421 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 480

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 540

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
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Db        541 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 600

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 660

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
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Db        661 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 720

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
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Db        721 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 780

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 840

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 900

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
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Db        901 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 960

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
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Db        961 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1020

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1080

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
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Db       1081 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1140

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1240
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Db       1141 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1180
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RESULT 9
HSU35232

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LOCUS       HSU35232                1180 bp    DNA     linear   PRI 14-NOV-1995
DEFINITION  Human neuropeptide Y4 receptor protein gene, complete cds.
ACCESSION   U35232
VERSION     U35232.1  GI:1063629
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1180)
  AUTHORS   Bard,J.A., Walker,M.W., Branchek,T.A. and Weinshank,R.L.
  TITLE     Cloning and functional expression of a human Y4 subtype receptor
            for pancreatic polypeptide, neuropeptide Y, and peptide YY
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  JOURNAL   J. Biol. Chem. 270 (45), 26762-26765 (1995)
  MEDLINE   96070761
   PUBMED   7592911
REFERENCE   2  (bases 1 to 1180)
  AUTHORS   Bard,J.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-1995) Jonathan A. Bard, Molecular Biology,
            Synaptic Pharmaceutical Corporation, 215 College Rd., Paramus, NJ
            07652, USA
FEATURES             Location/Qualifiers
     source          1. .1180
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="hp25a"
                     /tissue_type="placenta"
     5'UTR           1. .27
     CDS             28. .1155
                     /codon_start=1
                     /product="neuropeptide Y4 receptor protein"
                     /protein_id="AAC50280.1"
                     /db_xref="GI:1063630"
                     /translation="MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFI
                     VTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYT
                     IMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGI
                     VLIWVIACVLSLPFLANSILENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFL
                     LLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAV
                     LWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIK
                     ALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI"
     3'UTR           1156. .1180
ORIGIN

  Query Match             89.4%;  Score 1180;  DB 9;  Length 1180;
  Best Local Similarity   100.0%;  Pred. No. 4e-202;
  Matches 1180;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 60

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 120

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 180

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
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Db        181 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 240

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 300

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
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Db        301 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 360

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
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Db        361 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 420

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 480

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
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Db        481 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 540

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
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Db        541 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 600

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 660

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
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Db        661 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 720

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 780

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
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Db        781 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 840

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 900

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
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Db        901 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 960

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
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Db        961 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1020

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1080

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1140

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1240
               ||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1180


RESULT 10
AX548917
LOCUS       AX548917               1128 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 202 from Patent WO02061087.
ACCESSION   AX548917
VERSION     AX548917.1  GI:25813768
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 202 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1128
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             85.5%;  Score 1128;  DB 6;  Length 1128;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-193;
  Matches 1128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        88 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 147
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Db         1 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 60

Qy       148 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 207
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Db        61 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 120

Qy       208 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 267
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Qy       268 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 327
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Qy       388 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 447
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Qy       508 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 567
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Db       421 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 480

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Qy       628 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 687
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Qy       688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
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Qy       748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
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Qy       868 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 927
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Qy       928 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 987
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Db       841 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 900

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Qy      1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
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Qy      1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
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Qy      1168 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1215
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RESULT 11
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LOCUS       AY268432                1128 bp    DNA     linear   PRI 05-MAY-2003
DEFINITION  Homo sapiens pancreatic polypeptide receptor 1 (PPYR1) gene,
            complete cds.
ACCESSION   AY268432
VERSION     AY268432.1  GI:30385609
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Kopatz,S.A., Aronstam,R.S. and Sharma,S.V.
  TITLE     Isolation of complete coding sequence for neuropeptide Y receptor
            Y4 (NPY4R)/ pancreatic polypeptide receptor 1 PPYR1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1128)
  AUTHORS   Kopatz,S.A., Aronstam,R.S. and Sharma,S.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2003) Guthrie cDNA Resource Center, Guthrie
            Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA
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     source          1. .1128
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                     /note="G-protein coupled receptor; neuropeptide Y receptor
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ORIGIN

  Query Match           84.8%;  Score 1120;  DB 9;  Length 1128;
  Best Local Similarity   99.6%;  Pred. No. 2.4e-191;
  Matches 1123;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Db          1 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 60

Qy        148 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 207
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Qy        208 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 267
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Qy        328 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 387
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Qy        568 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 627
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Qy        688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
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Db        601 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 660

Qy        748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
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Qy        808 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 867
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Db        721 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 780

Qy        868 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 927
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Qy        928 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 987
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Db        841 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCATGGG 900

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Qy       1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
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Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
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Db       1021 CAGCAGAGCGCCCCCCTGGAGGAGTCAGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1080

Qy       1168 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1215
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Db       1081 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1128
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RESULT 12
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LOCUS       AY149475                1128 bp    DNA     linear   PRI 01-OCT-2003
DEFINITION  Macaca mulatta neuropeptide Y receptor 4 gene, complete cds.
ACCESSION   AY149475
VERSION     AY149475.1  GI:37359216
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Berglund,M.M., Schober,D.A., Esterman,M.A. and Gehlert,D.R.
  TITLE     The Rhesus Neuropeptide Y Receptor Y4: Cloning, Dimerization and
            Agonist Driven Internalization
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1128)
  AUTHORS   Berglund,M.M., Schober,D.A., Esterman,M.A. and Gehlert,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-2002) Neuroscience, Eli Lilly and Co., Lilly
            Corp. Center, Indianapolis, IN 46285, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             79.6%;  Score 1051.2;  DB 9;  Length 1128;
  Best Local Similarity   95.7%;  Pred. No. 5.6e-179;
  Matches 1080;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

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Db          1 ATGAACACCTCTCACCTCCTGGCCTTGCAGCTGCCAAAATCCCTACAGGGTGAAAACAGA 60

Qy        148 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 207
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Qy        388 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 447
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Db        301 TATACCATCATGGATTACTGGATCTTCGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 360
Qy        448 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 507
Db        361 CAGTGTGTGTCGGTGACGGTCTCTATCCTCTCGCTCGTCCTTGTGGCCCTGGAGAGGCAT 420
Qy        508 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 567
Db        421 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCTCAGGCTTACCTGGGGATT 480
Qy        568 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 627
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Qy        628 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 687
Db        541 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTC 600
Qy        688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
Db        601 TGTACTGAGTCCTGGCCACTGGCTCACCACCGCACCATCTATACCACCTTCCTCCTCCTC 660
Qy        748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
Db        661 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 720
Qy        808 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 867
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Db        781 AAGCAGGTCAATGTGGTGCTGGTGGCGATGGTGGTGGCCTTCGCTGTGCTCTGGCTGCCT 840
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Qy        988 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 1047
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Qy       1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
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Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
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Db       1081 GTCTCCAAAGTGTCCCTGAGGCTAAATGGCAGGTCCAATCCCATTTAA 1128
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RESULT 13
AB021678
LOCUS       AB021678               1796 bp    mRNA    linear   MAM 26-DEC-1998
DEFINITION  Sus scrofa gene for neuropeptide Y receptor type 4, complete cds.
ACCESSION   AB021678
VERSION     AB021678.1  GI:4062996
KEYWORDS    neuropeptide Y receptor type 4; NPY Y4.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 1796)
  AUTHORS   Ito,Y. and Minezawa,M.
  TITLE     Sus scrofa NPY Y4 gene for neuropeptide Y receptor type 4, complete
            cds [genomic]
  JOURNAL   Published Only in DataBase (1998)
REFERENCE   2  (bases 1 to 1796)
  AUTHORS   Ito,Y. and Minezawa,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-1998) Yoshiyasu Ito, National Institute of Animal
            Industry, Animal Genome Research Team; 2 Ikenodai, Kukizaki-machi,
            Inashiki-gun, Ibaragi 305-0901, Japan
            (E-mail:yoshiito@niai.affrc.go.jp, Tel:81-298-38-8627)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           74.4%;  Score 982.6;  DB 4;  Length 1796;
  Best Local Similarity  86.9%;  Pred. No. 1.1e-166;
  Matches 1092;  Conservative    0;  Mismatches  164;  Indels    1;  Gaps    1;

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Qy        185 ATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTG 244
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Qy        365 TCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCC 424
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Qy        425 TCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCG 484
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Qy        485 TCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCA 544
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Qy        545 TCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGC 604
Db        780 TCTCCCAGGCCTACCTGGGGATTGTGGTCATCTGGCTCATTGCCTGCTTCCTCTCCCTGC 839
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RESULT 14
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LOCUS       AF227955               1128 bp    DNA     linear   MAM 05-APR-2000
DEFINITION  Sus scrofa neuropeptide Y-family receptor Y4 gene, complete cds.
ACCESSION   AF227955
VERSION     AF227955.1  GI:7417237
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Wraith,A., Tornsten,A., Chardon,P., Harbitz,I., Chowdhary,B.P.,
            Andersson,L., Lundin,L.G. and Larhammar,D.
  TITLE     Evolution of the neuropeptide Y receptor family: gene and
            chromosome duplications deduced from the cloning and mapping of the
            five receptor subtype genes in pig
  JOURNAL   Genome Res. 10 (3), 302-310 (2000)
  MEDLINE   20187975
   PUBMED   10720571
REFERENCE   2  (bases 1 to 1128)
  AUTHORS   Wraith,A., Tornsten,A., Chardon,P., Harbitz,I., Chowdhary,B.P.,
            Andersson,L., Lundin,L.-G. and Larhammar,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2000) Neuroscience, Uppsala University, Box 593,
            Uppsala SE-75124, Sweden
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Qy        568 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 627
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DEFINITION  Cavia porcellus pancreatic polypeptide receptor Y4 gene, complete
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ACCESSION   AF072822
VERSION     AF072822.1  GI:4235258
KEYWORDS    .
SOURCE      Cavia porcellus (domestic guinea pig)
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1  (bases 1 to 1119)
  AUTHORS   Eriksson,H., Berglund,M.M., Holmberg,S.K., Kahl,U., Gehlert,D.R.
            and Larhammar,D.
  TITLE     The cloned guinea pig pancreatic polypeptide receptor Y4 resembles
            more the human Y4 than does the rat Y4
  JOURNAL   Regul. Pept. 75-76, 29-37 (1998)
  MEDLINE   99017377
   PUBMED   9802391
REFERENCE   2  (bases 1 to 1119)
  AUTHORS   Sharma,P.S., Holmberg,S.K., Eriksson,H., Beck-Sickinger,A.G.,
            Grundemar,L. and Larhammar,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1998) Neuroscience, Uppsala University, Box 593,
            Uppsala SE-75124, Sweden
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ORIGIN
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  Matches  949;  Conservative    0;  Mismatches  169;  Indels    9;  Gaps    1;

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Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
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Job time : 5337 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 11:55:42 ; Search time 582 Seconds
(without alignments)
9635.088 Million cell updates/sec

Title: US-09-430-775-1
Perfect score: 1320
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1210	91.7	1959	4	AAI14591	Aai14591 Probe #45
3	1210	91.7	1959	4	ABA25958	Aba25958 Probe #44
4	1210	91.7	1959	4	AAK29996	Aak29996 Human bon
5	1180	89.4	1180	7	ACA56463	Aca56463 Human sig
6	1128	85.5	1128	4	AAD12802	Aad12802 Human neu
7	1128	85.5	1128	7	ABZ42706	Abz42706 Human neu
8	959.4	72.7	983	4	AAI23787	Aai23787 Probe #13
9	959.4	72.7	983	4	ABA35852	Aba35852 Probe #14
10	959.4	72.7	983	4	AAK43019	Aak43019 Human bon
11	811.2	61.5	1440	2	AAQ94172	Aaq94172 Neuropept
12	807.8	61.2	1500	6	AAI72366	Aai72366 NPY4-R ge
13	278.6	21.1	2280	2	AAT36127	Aat36127 Mouse neu
14	278.6	21.1	2281	6	AAI72369	Aai72369 NPY6-R ge
15	266	20.2	1499	2	AAT36128	Aat36128 Human neu
16	257.6	19.5	1152	3	AAA62588	Aaa62588 Rhesus Y1
17	257.6	19.5	1152	3	AAA62587	Aaa62587 Rhesus Y1
18	257.6	19.5	1155	9	AAD62456	Aad62456 Human neu
19	257.6	19.5	1605	4	AAF86517	Aaf86517 Human oli
20	257.6	19.5	1605	4	AAF77580	Aaf77580 Human neu
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23	257.6	19.5	1605	6	ABN84250	Abn84250 Human neu
24	257.6	19.5	1605	7	ACA56633	Aca56633 Human sig
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27	257.6	19.5	2624	2	AAQ40768	Aaq40768 Human NPY
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33	257.6	19.5	2752	7	ABZ42794	Abz42794 Human neu
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36	255.6	19.4	1957	7	ABZ42793	Abz42793 Human neu
37	254	19.2	1952	4	AAD12804	Aad12804 Human neu
38	253.8	19.2	1401	4	AAD12799	Aad12799 Human neu
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40	236.8	17.9	924	2	AAT32987	Aat32987 Mouse neu
41	173.6	13.2	595	2	AAV41690	Aav41690 Nucleotid
42	159.8	12.1	3721	6	AAS16903	Aas16903 Human neu
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44	157.6	11.9	1174	2	AAT87889	Aat87889 Human hyp
45	156	11.8	1110	2	AAT18371	Aat18371 Human pit

ALIGNMENTS

RESULT 1
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ID AAQ94171 standard; DNA; 1320 BP.
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AC AAQ94171;
XX
DT 07-DEC-1995 (first entry)
XX
DE Neuropeptide Y/peptide YY/pancretic polypeptide receptor (Y4).
XX
KW Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;
KW therapeutic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 88. .1212
FT /*tag= a
XX
PN WO9517906-A1.
XX
PD 06-JUL-1995.
XX
PF 28-DEC-1994; 94WO-US014436.
XX
PR 28-DEC-1993; 93US-00176412.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Bard JA, Walker MW, Branchek T, Weinshank RL;
XX
DR WPI; 1995-246190/32.
DR P-PSDB; AAR79119.
XX
PT New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -
PT useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc.
XX
PS Claim 8; Fig 1; 154pp; English.
XX
CC The sequence encodes a human neuropeptide Y/peptide YY/pancreatic
CC polypeptide (Y4) receptor, which can be expressed from a vector adapted
CC for expression in a bacterial, mammalian, yeast or insect cell,
CC specifically pcEXV-Y4 (ATCC 75631) and pcEXV-rY4 expression in COS-7,
CC LM(tk)- or NIH3T3 cells. The Y4 receptor can be used to screen drugs
CC which bind to it, specifically to find ligands (agonists or antagonists)
CC which bind to it. The ligands can be used to treat abnormalities,

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CC   specifically the antagonists can be used to treat amnesia, feeding
CC   disorders, epilepsy, hypertension, sleeping disorders or pain. Antisense
CC   oligonucleotides to the DNA can be used in compositions to decrease the
CC   activity of Y4 receptor, especially in transgenic non-human mammals
XX
SQ   Sequence 1320 BP; 257 A; 417 C; 322 G; 324 T; 0 U; 0 Other;

  Query Match             99.6%;  Score 1315.2;  DB 2;  Length 1320;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-309;
  Matches 1317;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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RESULT 2
AAI14591
ID   AAI14591 standard; DNA; 1959 BP.
XX
AC   AAI14591;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #4524 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000670.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human cervical epithelial cells.
XX
PS   Claim 25; SEQ ID NO 4524; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging of
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CC   diseases of the cervix, notably cervical cancer. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1959 BP; 402 A; 554 C; 494 G; 494 T; 0 U; 15 Other;

  Query Match             91.7%;  Score 1210;  DB 4;  Length 1959;
  Best Local Similarity   96.9%;  Pred. No. 8.8e-284;
  Matches 1279;  Conservative    0;  Mismatches   34;  Indels    7;  Gaps    5;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         88 AGTATTGTTTGTCTGTTTGCCTTGTA-GGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 146

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 206

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 266

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 326

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 386

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTNN 446

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
              ||    || ||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        447 CTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 506

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 566

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 626

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 686

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 746

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
              |||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db        747 CTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNTCACCACCGC 806

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        807 ACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGNTTCATNTTG 866

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 926

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 986

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||

Db        987 GTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 1046

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       1047 CATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1106

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
              |||||||||||||| |||||||||||||||||||||||||| |||||||||||||| ||
Db       1107 ATGGCCTCCACCTGTGTCAACCCATTCATCTATGGCTTTCT-AACACCAACTTCAAG-AG 1164

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
              ||||  |||||||||||||||||||||||||     | ||||||||||||||  ||||||
Db       1165 GAGAATAAGGCCCTGGTGCTGACTTGCCAG--AGAGGGCCCCCTGGAGGAGTAAGAGCAT 1222

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1282

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db       1283 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGGTTTTC 1342

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
              |||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db       1343 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCC--AGATTCCTGGCTTTCTG 1400
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RESULT 3
ABA25958
ID   ABA25958 standard; DNA; 1959 BP.
XX
AC   ABA25958;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #4424 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000666.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts.
XX
PS   Claim 1; SEQ ID NO 4424; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
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CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1959 BP; 402 A; 554 C; 494 G; 494 T; 0 U; 15 Other;

  Query Match             91.7%;  Score 1210;  DB 4;  Length 1959;
  Best Local Similarity   96.9%;  Pred. No. 8.8e-284;
  Matches 1279;  Conservative    0;  Mismatches   34;  Indels    7;  Gaps    5;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
Db         88 AGTATTGTTTGTCTGTTTGCCTTGTA-GGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 146

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
Db        147 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 206

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
Db        207 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 266

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
Db        267 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 326

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
Db        327 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 386

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
Db        387 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTNN 446

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
Db        447 CTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 506

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
Db        507 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 566

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
Db        567 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 626

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
Db        627 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 686

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
Db        687 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 746

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
Db        747 CTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNTCACCACCGC 806

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
Db        807 ACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGNTTCATNTTG 866

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
Db        867 GTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 926

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
Db        927 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 986

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
Db        987 GTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 1046

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
Db       1047 CATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1106

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
Db       1107 ATGGCCTCCACCTGTGTCAACCCATTCATCTATGGCTTTCT-AACACCAACTTCAAG-AG 1164

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
Db       1165 GAGAATAAGGCCCTGGTGCTGACTTGCCAG--AGAGGGCCCCCTGGAGGAGTAAGAGCAT 1222

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
Db       1223 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1282

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
Db       1283 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGGTTTTC 1342

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
Db       1343 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCC--AGATTCCTGGCTTTCTG 1400

RESULT 4
AAK29996
ID   AAK29996 standard; DNA; 1959 BP.
XX
AC   AAK29996;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 4553.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 4553; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
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CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention
XX
SQ   Sequence 1959 BP; 402 A; 554 C; 494 G; 494 T; 0 U; 15 Other;

  Query Match           91.7%;  Score 1210;  DB 4;  Length 1959;
  Best Local Similarity 96.9%;  Pred. No. 8.8e-284;
  Matches 1279;  Conservative    0;  Mismatches   34;  Indels    7;  Gaps    5;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         88 AGTATTGTTTGTCTGTTTGCCTTGTA-GGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 146

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 206

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 266

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 326

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 386

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTNN 446

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
              ||   || ||| || ||||||||||||||||||||||||||||||||||||||||||||
Db        447 CTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 506

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 566

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 626

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 686

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 746

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
              |||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Db        747 CTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNTCACCACCGC 806

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
              ||||| |||||||||||||||||| |||||||||||||||||||||| ||||| ||
Db        807 ACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGNTTCATNTTG 866

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
              |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Db        867 GTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 926

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 986

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        987 GTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 1046

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1047 CATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1106

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
              |||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||| ||
Db       1107 ATGGCCTCCACCTGTGTCAACCCATTCATCTATGGCTTTCT-AACACCAACTTCAAG-AG 1164

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
              ||||  |||||||||||||||||||||||||  | ||||||||||||  ||||||
Db       1165 GAGAATAAGGCCCTGGTGCTGACTTGCCAG--AGAGGGCCCCCTGGAGGAGTAAGAGCAT 1222

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1223 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1282

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db       1283 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGGTTTTC 1342

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1343 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCC--AGATTCCTGGCTTTCTG 1400
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RESULT 5
ACA56463
ID   ACA56463 standard; cDNA; 1180 BP.
XX
AC   ACA56463;
XX
DT   06-JUN-2003  (first entry)
XX
DE   Human signalling pathway polynucleotide probe SEQ ID NO 1061.
XX
KW   Human; probe; ss; array element; Parkinson's disease;
KW   signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW   immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS   Homo sapiens.
XX
PN   US6500938-B1.
XX
PD   31-DEC-2002.
XX
PF   30-JAN-1998;   98US-00016434.
XX
PR   30-JAN-1998;   98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J,  Seilhamer JJ;
XX
DR   WPI; 2003-352189/33.
XX
PT   Combination of polynucleotide probes, useful as array elements in a
PT   microarray for monitoring the expression of a number of target
PT   polynucleotides.
XX
PS   Claim 1; SEQ ID NO 1061; 65pp; English.
XX
CC   The invention relates to a combination which, comprises a number of
CC   polynucleotide probes comprising a sequence selected from one of the 1490
CC   sequences mentioned in the specification. The combination is useful as an
CC   array element in a microarray for monitoring the expression of a number
CC   of target polynucleotides. The microarray is particularly useful in the
CC   diagnosis and treatment of cancer and immunopathology and neuropathology.
CC   The microarray is useful in diagnostics and treatment regimens, drug
CC   discovery and development, toxicological and carcinogenicity studies,
CC   forensics and pharmacogenomics. The microarray is also useful for
CC   monitoring progression of diseases and for developing sophisticated
CC   profiles for the effects of currently available therapeutic drugs. The
CC   combination is also useful for purifying a subpopulation of mRNAs, cDNAs
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CC   and genomic fragments and in research and diagnostic applications. The
CC   array can detect changes in expression in a large number of genes coding
CC   for different signaling pathway populations which can be used to diagnose
CC   various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC   immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC   and Parkinson's disease. The present sequence represents a polynucleotide
CC   probe of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ   Sequence 1180 BP; 234 A; 382 C; 285 G; 279 T; 0 U; 0 Other;

  Query Match             89.4%;  Score 1180;  DB 7;  Length 1180;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-276;
  Matches 1180;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 60

Qy         121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 120

Qy         181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 180

Qy         241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 240

Qy         301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 300

Qy         361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 360

Qy         421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 420

Qy         481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 480

Qy         541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 540

Qy         601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 600

Qy         661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 660

Qy         721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 720

Qy         781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 780

Qy         841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 840

Qy         901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 900

Qy         961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 960

Qy        1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1020

Qy        1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1080

Qy        1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1140

Qy        1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1240
               |||||||||||||||||||||||||||||||||||||||
Db        1141 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1180
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RESULT 6
AAD12802
ID   AAD12802 standard; DNA; 1128 BP.
XX
AC   AAD12802;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human neuropeptide Y (NPY) Y4 receptor DNA.
XX
KW   Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;
KW   cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
KW   fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
KW   osteopenia; bone metastasis; neurotransmitter; osteogenic;
KW   NPY Y4 receptor; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1128
FT                   /*tag=  a
FT                   /product= "Human neuropeptide Y (NPY) Y4 receptor"
XX
PN   WO200153477-A1.
XX
PD   26-JUL-2001.
XX
PF   22-JAN-2001; 2001WO-US002040.
XX
PR   20-JAN-2000; 2000US-00489872.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (AMLI/) AMLING M.
XX
PI   Amling M,  Karsenty G,  Ducy P;
XX
DR   WPI; 2001-488709/53.
DR   P-PSDB; AAE06691.
XX
PT   Treating or preventing reduced bone mass, e.g. osteoporosis, by reducing
PT   the level of neuropeptide Y activity in blood or cerebrospinal fluid.
XX
PS   Example 7; Page 86; 102pp; English.
XX
CC   The present invention relates to a method for treatment or prevention of
CC   bone diseases characterised by loss of bone mass, comprises administering
CC   to a mammal a compound that lowers the level of neuropeptide Y (NPY) in
CC   the serum or cerebrospinal fluid (CSF) or a compound that lowers the
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CC   level of inositol phosphate (IP) or extracellular signal-regulated kinase
CC   (ERK). The method is specifically used to treat (including by gene
CC   therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may
CC   also be used e.g., in cases of fractures or bone metastases. These
CC   diseases may also be diagnosed by detecting elevated NPY levels,
CC   including monitoring of treatment, assessing efficacy of compounds in
CC   clinical trials and for identifying subjects at risk. The present
CC   sequence is a human NPY Y4 receptor DNA
XX
SQ   Sequence 1128 BP; 225 A; 364 C; 276 G; 263 T; 0 U; 0 Other;

  Query Match           85.5%;  Score 1128;  DB 4;  Length 1128;
  Best Local Similarity  100.0%;  Pred. No. 6.1e-264;
  Matches 1128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 60

Qy        148 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 207
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 120

Qy        208 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 180

Qy        268 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 327
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 240

Qy        328 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 387
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 300

Qy        388 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 447
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 360

Qy        448 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 507
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 420

Qy        508 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 567
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 480

Qy        568 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 627
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 540

Qy        628 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 687
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 600

Qy        688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 660

Qy        748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 720

Qy        808 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 867
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 780

Qy        868 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 927
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 840

Qy        928 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 987
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 900

Qy        988 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 1047
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 960

Qy       1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1020

Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1080

Qy       1168 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1215
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1128
```

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RESULT 7
ABZ42706
ID   ABZ42706 standard; DNA; 1128 BP.
XX
AC   ABZ42706;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human neuropeptide Y receptor type 4 nucleotide SEQ ID NO:202.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,  Roush CL,  Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81859.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
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CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1128 BP; 225 A; 364 C; 276 G; 263 T; 0 U; 0 Other;

  Query Match             85.5%;  Score 1128;  DB 7;  Length 1128;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-264;
  Matches 1128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 60

Qy        148 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 207
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 120

Qy        208 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 180

Qy        268 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 327
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 240

Qy        328 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 387
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 300

Qy        388 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 447
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 360

Qy        448 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 507
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 420

Qy        508 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 567
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 480

Qy        568 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 627
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 540

Qy        628 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 687
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 600

Qy        688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 660

Qy        748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 720

Qy        808 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 867
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 780

Qy        868 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 927
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 840

Qy        928 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 987
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 900

Qy        988 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 1047
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 960

Qy       1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1020

Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1080

Qy       1168 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1215
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1128


RESULT 8
AAI23787
ID   AAI23787 standard; DNA; 983 BP.
XX
AC   AAI23787;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #13720 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000670.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human cervical epithelial cells.
XX
PS   Claim 25; SEQ ID NO 13720; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
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CC   expression, the probes are therefore useful in grading and/or staging of
CC   diseases of the cervix, notably cervical cancer. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 983 BP; 188 A; 300 C; 239 G; 242 T; 0 U; 14 Other;

  Query Match             72.7%;  Score 959.4;  DB 4;  Length 983;
  Best Local Similarity   98.0%;  Pred. No. 5.3e-223;
  Matches  963;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         52 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 60

Qy        112 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 120

Qy        172 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 180

Qy        232 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 240

Qy        292 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 300

Qy        352 CTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATC 411
              |||||||  ||     || ||| || ||||||||||||||||||||||||||||||||||||
Db        301 CTCATGTNNCTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATC 360

Qy        412 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 420

Qy        472 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 480

Qy        532 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 540

Qy        592 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 600

Qy        652 TCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCT 711
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||| |
Db        601 TCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNT 660

Qy        712 CACCACCGCACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGC 771
              |||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||
Db        661 CACCACCGCACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGN 720

Qy        772 TTCATCCTGGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTT 831
              |||||  |||||||||||||||||| |||||| ||||||||||||||||||||||||||
Db        721 TTCATNTTGGTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTT 780

Qy        832 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 840

Qy        892 GTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 951
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        841 GTGATGGTGGTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 900

Qy        952 GACTGGCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCAC 1011
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        901 GACTGGCACCATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCAC 960

Qy       1012 TTGCTTGCCATGGCCTCCACCTG 1034
              |||||||||||||||||||||||
Db        961 TTGCTTGCCATGGCCTCCACCTG 983


RESULT 9
ABA35852
ID   ABA35852 standard; DNA; 983 BP.
XX
AC   ABA35852;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #14318 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000666.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts.
XX
PS   Claim 4; SEQ ID NO 14318; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 983 BP; 188 A; 300 C; 239 G; 242 T; 0 U; 14 Other;

  Query Match             72.7%;  Score 959.4;  DB 4;  Length 983;
  Best Local Similarity   98.0%;  Pred. No. 5.3e-223;
  Matches  963;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         52 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 60

Qy        112 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCCTGGGCACCCCATAC 120

Qy        172 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 180

Qy        232 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 240

Qy        292 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 300

Qy        352 CTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATC 411
              |||||||  ||    || ||| || ||||||||||||||||||||||||||||||||||||
Db        301 CTCATGTNNCTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATC 360

Qy        412 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 420

Qy        472 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 480

Qy        532 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 540

Qy        592 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 600

Qy        652 TCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCT 711
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |
Db        601 TCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNT 660

Qy        712 CACCACCGCACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGC 771
              |||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||
Db        661 CACCACCGCACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGN 720

Qy        772 TTCATCCTGGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTT 831
              |||||  |||||||||||||||||||||| ||||| ||||||||||||||||||||||||
Db        721 TTCATNTTGGTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTT 780

Qy        832 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 840

Qy        892 GTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 951
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        841 GTGATGGTGGTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 900

Qy        952 GACTGGCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCAC 1011
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        901 GACTGGCACCATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCAC 960

Qy       1012 TTGCTTGCCATGGCCTCCACCTG 1034
              |||||||||||||||||||||||
Db        961 TTGCTTGCCATGGCCTCCACCTG 983


RESULT 10
AAK43019
ID   AAK43019 standard; DNA; 983 BP.
XX
AC   AAK43019;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 17576.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 17576; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention
XX
SQ   Sequence 983 BP; 188 A; 300 C; 239 G; 242 T; 0 U; 14 Other;

  Query Match           72.7%;  Score 959.4;  DB 4;  Length 983;
  Best Local Similarity  98.0%;  Pred. No. 5.3e-223;
  Matches  963;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         52 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 60

Qy        112 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 120

Qy        172 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 180

Qy        232 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 240

Qy        292 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 300

Qy        352 CTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATC 411
              |||||||  ||    || ||| || ||||||||||||||||||||||||||||||||||||
Db        301 CTCATGTNNCTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATC 360

Qy        412 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 420

Qy        472 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 480

Qy        532 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 540

Qy        592 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 600

Qy        652 TCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCT 711
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |
Db        601 TCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNT 660

Qy        712 CACCACCGCACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGC 771
              |||||||||||||| |||||||||||||||||||| |||||||||||||||||||||||
Db        661 CACCACCGCACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGN 720

Qy        772 TTCATCCTGGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTT 831
              |||||  |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        721 TTCATNTTGGTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTT 780

Qy        832 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 840

Qy        892 GTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTGATGGTGGTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 900

Qy        952 GACTGGCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCAC 1011
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 GACTGGCACCATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCAC 960

Qy       1012 TTGCTTGCCATGGCCTCCACCTG 1034
              |||||||||||||||||||||||
Db        961 TTGCTTGCCATGGCCTCCACCTG 983
```

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RESULT 11
AAQ94172
ID   AAQ94172 standard; DNA; 1440 BP.
XX
AC   AAQ94172;
XX
DT   09-DEC-1995  (first entry)
XX
DE   Neuropeptide Y/peptide YY/pancretic polypeptide receptor (Y4).
XX
KW   Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;
KW   therapeutic; ss.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   CDS             178. .1306
FT                   /*tag=  a
XX
PN   WO9517906-A1.
XX
PD   06-JUL-1995.
XX
PF   28-DEC-1994;   94WO-US014436.
XX
PR   28-DEC-1993;   93US-00176412.
XX
PA   (SYNA-) SYNAPTIC PHARM CORP.
XX
PI   Bard JA,  Walker MW,  Branchek T,  Weinshank RL;
XX
DR   WPI; 1995-246190/32.
DR   P-PSDB; AAR79120.
XX
PT   New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -
PT   useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc.
XX
PS   Claim 12; Fig 3; 154pp; English.
XX
CC   The sequence encodes a rat neuropeptide Y/peptide YY/pancreatic
CC   polypeptide (Y4) receptor, which can be expressed from a vector adapted
CC   for expression in a bacterial, mammalian, yeast or insect cell,
CC   specifically pcEXV-Y4 (ATCC 75631) and pcEXV-rY4 expression in COS-7,
CC   LM(tk)- or NIH3T3 cells. The Y4 receptor can be used to screen drugs
CC   which bind to it, specifically to find ligands (agonists or antagonists)
CC   which bind to it. The ligands can be used to treat abnormalities,
CC   specifically the antagonists can be used to treat amnesia, feeding
CC   disorders, epilepsy, hypertension, sleeping disorders or pain. Antisense
CC   oligonucleotides to the DNA can be used in compositions to decrease the
CC   activity of Y4 receptor, especially in transgenic non-human mammals
XX
SQ   Sequence 1440 BP; 292 A; 433 C; 312 G; 403 T; 0 U; 0 Other;
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  Query Match             61.5%;  Score 811.2;  DB 2;  Length 1440;
  Best Local Similarity   78.7%;  Pred. No. 6.1e-187;
  Matches  981;  Conservative    0;  Mismatches  263;  Indels    2;  Gaps    1;

Qy         72 TCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCC 131
              |||| |||| |||| |||| |||||||| ||| |||||  ||    ||   || | |
Db        162 TCTTCTCACACCCACCATGAATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCCT 221

Qy        132 ACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCA 191
              ||||||| | ||  | | ||| || ||||   |||  || ||  |||||||    |||||
Db        222 ACAAGGTAAGAATGGGACCAACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCA 281

Qy        192 GGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGG 251
              |||||| |  ||  || ||| ||||||| ||||  |||||||| |||||||  ||| ||||
Db        282 GGATTCGGCAGATCTGTTGGCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGG 341

Qy        252 GGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGT 311
              |||||| || |||||||||| |||| | ||||||     ||||| ||||| ||  |||| ||
Db        342 GGTCCTAGGAAACCTCTGCTTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGT 401

Qy        312 GACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCA 371
              ||||||||| || || |||||||||||||||||||||||||||||||| ||| |||||||
Db        402 GACCAACCTACTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCA 461

Qy        372 GCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAA 431
              |||||| || | |  |||||||||||||||||||||||||||| || ||  ||| |||||
Db        462 GCCGCTCACGGTCACCTACACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAA 521

Qy        432 GATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGT 491
              |||||    | |||||||||| |||||||||| |||||||||||||| || ||||| ||
Db        522 GATGTTAACGTTCATCCAGTGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGT 581

Qy        492 GGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACA 551
              |||||||||||||||| |||||||| |||||||| || |||||||| |||||||| || ||
Db        582 GGCCCTGGAGAGGCACCAGCTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCCA 641

Qy        552 GGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCT 611
              |||||||||||||||||||| |||||||| ||||| | ||| |||||||| ||||||||||
Db        642 GGCCTACCTGGGGATTGTGGTCATCTGGTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCT 701

Qy        612 GGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCT 671
              |||||| |||||||||  |  |||||||| | |||||||| |||| | ||||||| ||
Db        702 GGCCAATAGCATCCTGAACGACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCT 761

Qy        672 GGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACAC 731
              || ||| ||||| |||||     | |||||||  |  || ||||||||| ||||||||||
Db        762 GGAAGACAAGGTTGTCTGCTTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACAC 821

Qy        732 CACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGC 791
              |||||| ||||| |||||||| |||||| |||| |||| ||||||||||||||||| ||
Db        822 CACCTTTCTGCTGCTCTTCCAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACAT 881

Qy        792 ACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTT 851
               || ||||| | |||||||||||||||| |||| | ||| |||| |  ||| | |||||
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Db        882 GCGTATCTATCAGCGCCTGCAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTC 941

Qy        852 GCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGC 911

Db        942 ACGAGTGGGGCAGATGAAGCGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGC 1001

Qy        912 CGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCAT 971

Db       1002 AGTTCTCTGGCTGCCCCTGCATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCAT 1061

Qy        972 CCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCAC 1031

Db       1062 CCCTGCTTGCCATGGCAACCTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCAC 1121

Qy       1032 CTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGC 1091

Db       1122 CTGTGTCAACCCTTTCATCTATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGC 1181

Qy       1092 CCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTC 1151

Db       1182 TCTGGTTCTGACCTGCCGTTGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTC 1241

Qy       1152 CACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCAT 1211

Db       1242 CACTGTGCACACGGACCTCTCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCAT 1301

Qy       1212 TTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTAGCTAA 1271

Db       1302 GTAGTCATGTCTAGG--CTCTTCCGCCATTTTCTTTCGACACACCCTTTCACTGAGCTAA 1359

Qy       1272 GTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTT 1317

Db       1360 GTAGACACAATGCAAGCTGTGGTATCATCCTGCCATTTCTGGTCTT 1405


RESULT 12
AAI72366
ID   AAI72366 standard; DNA; 1500 BP.
XX
AC   AAI72366;
XX
DT   15-MAY-2002  (first entry)
XX
DE   NPY4-R gene.
XX
KW   Gene; non-human; transgenic; mouse; G protein-coupled receptor; GPCR;
KW   gene therapy; neurological disease; neuropsychological disease; KOR3;
KW   psychotic illness; DEZ receptor; CB2R; adrenomedullin receptor; CRFR2;
KW   corticotropin-releasing factor receptor; neuropeptide Y receptor gene;
KW   N-formylpeptide receptor-like 3; FPRL3; NPY6-R; kappa-3 opiate receptor;
KW   metabotropic glutamate receptor; mGluR8; MAS receptor; NPY4-R;
KW   targeting arm; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 339. .440
FT                   /*tag=  a
FT                   /note= "Deleted in targeting construct"
XX
PN   WO200203789-A2.
XX
PD   17-JAN-2002.
XX
PF   06-JUL-2001; 2001WO-US021498.
XX
PR   06-JUL-2000; 2000US-0216108P.
PR   06-JUL-2000; 2000US-0216250P.
PR   06-JUL-2000; 2000US-0216252P.
PR   06-JUL-2000; 2000US-0216253P.
PR   06-JUL-2000; 2000US-0216254P.
PR   06-JUL-2000; 2000US-0216259P.
PR   06-JUL-2000; 2000US-0216260P.
PR   06-JUL-2000; 2000US-0216271P.
PR   06-JUL-2000; 2000US-0216473P.
PR   06-JUL-2000; 2000US-0216475P.
PR   19-JUL-2000; 2000US-0219403P.
PR   27-JUL-2000; 2000US-0221473P.
PR   27-JUL-2000; 2000US-0221474P.
PR   27-JUL-2000; 2000US-0221484P.
PR   27-JUL-2000; 2000US-0221490P.
PR   27-JUL-2000; 2000US-0221497P.
PR   07-AUG-2000; 2000US-0223625P.
PR   06-DEC-2000; 2000US-0251815P.
PR   16-JAN-2001; 2001US-0262137P.
PR   16-JAN-2001; 2001US-0262138P.
PR   29-MAR-2001; 2001US-0280264P.
PR   26-JUN-2001; 2001US-0300929P.
XX
PA   (DELT-) DELTAGEN INC.
XX
PI   Allen KD,  Brennan TJ;
XX
DR   WPI; 2002-154854/20.
XX
PT   Novel non-human transgenic animal, preferably transgenic mice comprising
PT   disruptions in target G protein-coupled receptor gene, useful for
PT   identifying an agent that modulates expression or function of target
PT   gene.
XX
PS   Example 6; Fig 16; 93pp; English.
XX
CC   This sequence represents the neuropeptide Y receptor gene (NPY4-R). The
CC   targeting arms (AAI72367-68) were used to disrupt this gene. The
CC   resulting sequence was used in the production of a non-human transgenic
CC   animal, preferably a mouse, with targeted G protein-coupled receptor gene
CC   disruption in the NPY4-R gene. The transgenic animal is useful for
CC   identifying an agent that modulates the expression or function of the
CC   target gene, by administering an agent, and determining whether the
CC   expression or function of the target is modulated. It is also useful for
CC   testing the efficacy of proposed genetic and pharmacological therapies
CC   for human genetic diseases, such as neurological, neuropsychological or
CC   psychotic illnesses. The transgenic mice are useful as models for
CC   diseases, disorders or conditions associated with phenotypes relating to
CC   a disruption in a target, and to identify drugs, pharmaceuticals,
CC   therapies and interventions which may be effective in treating a disease
CC   or other phenotypic characteristics of the animal
XX
SQ   Sequence 1500 BP; 320 A; 428 C; 312 G; 440 T; 0 U; 0 Other;

  Query Match             61.2%;  Score 807.8;  DB 6;  Length 1500;
  Best Local Similarity   76.5%;  Pred. No. 4.1e-186;
  Matches 1003;  Conservative    0;  Mismatches  307;  Indels    1;  Gaps    1;

Qy          7 GTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCC 66

Db        123 GTTCCATTTGTTTGTTTTGCAGGCTGCATCTCTGAAGTAGGCCCTTTACTCCTGGAGTTC 182

Qy         67 TGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAA 126

Db        183 CCGGATCTTCTCACACCTACCATGAATACCTCTCATTTCTTGGCCCCTCTCTTCCCAGGA 242

Qy        127 TCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACAT 186

Db        243 TCCCTACAGGGTAAGAATGGGACCAATCCATTGGATTCCCCCTATAATTTCTCTGATGGC 302

Qy        187 TGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTC 246

Db        303 TGCCAGGATTCGGCAGAACTGTTGGCCTTCATCATCACCACCTACAGCATTGAGACCATC 362

Qy        247 GTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCC 306

Db        363 TTAGGGGTCCTGGGAAACCTCTGCTTGATATTTGTGACCACAAGACAAAAGGAAAAGTCC 422

Qy        307 AACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTC 366
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Db        423 AATGTGACCAACCTACTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCATC 482
Qy        367 TGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTC 426
Db        483 TGCCAACCACTCACAGTCACCTACACCATCATGGATTACTGGATCTTTGGTGAAGTCCTT 542
Qy        427 TGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTC 486
Db        543 TGCAAGATGTTAACTTTCATCCAGTGTATGTCAGTGACAGTCTCCATCCTCTCACTGGTC 602
Qy        487 CTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATC 546
Db        603 CTTGTGGCCCTGGAGAGACACCAGCTCATTATCAATCCAACAGGCTGGAAACCCAGTATT 662
Qy        547 TCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCC 606
Db        663 TTCCAGGCCTACCTGGGGATTGTGGTCATCTGGTTCATCTCTTGTTTCCTTTCCTTGCCG 722
Qy        607 TTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAG 666
Db        723 TTCCTGGCCAACAGCACCCTGAATGACCTCTTCCACTACAACCACTCTAAGGTTGTAGAG 782
Qy        667 TTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATC 726
Db        783 TTTCTGGAAGACAAGGTCGTCTGCTTTGTGTCCTGGTCTTCAGATCACCACCGTCTCATC 842
Qy        727 TACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGT 786
Db        843 TATACCACCTTTCTGCTGCTCTTTCAGTACTGCATCCCTCTAGCCTTCATCCTGGTCTGC 902
Qy        787 TATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTAC 846
Db        903 TACATACGCATCTACCAGCGCCTGCAGAGGCAGAAGCATGTGTTCCATGCGCACGCTTGC 962
Qy        847 AGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCC 906
Db        963 AGCTCACGAGCGGGGCAGATGAAGCGGATCAACAGCATGCTCATGACAATGGTGACTGCC 1022
Qy        907 TTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAG 966
Db       1023 TTTGCAGTTCTCTGGCTACCCCTGCATGTGTTCAACACTCTGGAGGACTGGTACCAGGAA 1082
Qy        967 GCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCC 1026
Db       1083 GCCATCCCTGCTTGCCATGGCAACCTCATCTTCTTGATGTGCCACCTGTTGGCCATGGCT 1142
Qy       1027 TCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATC 1086
Db       1143 TCCACCTGTGTCAACCCTTTCATCTATGGCTTTCTCAACATCAACTTCAAGAAGGATATC 1202
Qy       1087 AAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCC 1146
Db       1203 AAGGCTCTGGTGCTGACCTGCCATTGCAGGTCACCTCAAGGGGAGTCTGAGCATCTGCCC 1262
Qy       1147 CTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAAT 1206
Db       1263 CTGTCCACTGTTCACACGGACCTCTCCAAGGGATCGATGAGGATGGGTAGCAAGTCTAAC 1322
Qy       1207 CCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTA 1266
Db       1323 TTCATATAGTTGTGTCT-GGGCTTTTCCCTACCATTTTTTTTGACACATCCTTTCACTTA 1381
Qy       1267 GCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTT 1317
Db       1382 GTTAAGAAGACACATTGCAGGCTGTGATAGCATCCTGTCATTTCTGGCTTT 1432

RESULT 13
AAT36127
ID   AAT36127 standard; DNA; 2280 BP.
XX
AC   AAT36127;
XX
DT   25-OCT-1996  (first entry)
XX
DE   Mouse neuropeptide Y Yx receptor DNA.
XX
KW   Neuropeptide Y Yx receptor; NPY Yx; G-protein coupled receptor; obesity;
KW   diabetes; cardiac vasospasm; Parkinson's disease; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             822. .1937
FT                   /*tag=  a
XX
PN   WO9623809-A1.
XX
PD   08-AUG-1996.
XX
PF   30-JAN-1996;   96WO-US001444.
XX
PR   03-FEB-1995;   95US-00383746.
PR   03-APR-1995;   95US-00415818.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Cascieri MA,  Linemeyer DL,  Macneil DJ,  Shiao L,  Strader C;
PI   Weinberg DH,  Tan CP;
XX
DR   WPI; 1996-371369/37.
DR   P-PSDB; AAW02099.
XX
PT   DNA mol. encoding neuro:peptide Y Yx receptor - useful in assays to
PT   identify cpds. which bind to receptor, useful to treat, e.g. obesity,
PT   diabetes, cardiac vasospasm and Parkinson's disease.
XX
PS   Claim 1; Page 46-49; 65pp; English.
XX
CC   A PstI fragment (AAT36127) of pVE2841 codes for mouse neuropeptide Y
CC   subtype Yx (NPY Yx) receptor (AAW02099). It was obtd. from a mouse cosmid
CC   library using a probe generated by PCR amplification (see also AAT36131-
CC   32) of NPY Y1 receptor cDNA. Vectors were constructed to allow expression
CC   of the murine NPY Yx receptor DNA in mammalian (COS-7) cells. The
CC   recombinant receptor, or transformed host cells, can be used to screen
CC   for cpds. that modulate the function of the receptor, or modulate the
CC   expression of nucleic acids encoding the receptor. Such cpds. are useful
CC   for treating a variety of disease conditions
XX
SQ   Sequence 2280 BP; 695 A; 466 C; 460 G; 659 T; 0 U; 0 Other;

  Query Match             21.1%;  Score 278.6;  DB 2;  Length 2280;
  Best Local Similarity   53.2%;  Pred. No. 1.8e-57;
  Matches  637;  Conservative    0;  Mismatches  554;  Indels    6;  Gaps    2;

Qy         24 GTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTTCACATC 83
Db        740 GTTGTCCCTCAAGAACCAATGGCCAAACATCCACTGAGGATACACGGAAGCTTAGAAAAT 799
Qy         84 CACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAA 143
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Qy        144 CAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGA 203
Db        860 CAGTGGCAAGAGCAACAACTCGGCATTTTTCTACTTTGAATCCTGCCAACCCCCTTTTCT 919
Qy        204 CGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAA 263
Db        920 AGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTAATCATGGGCATTTTTGGAAA 979
Qy        264 CCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCC---AACGTGACCAACCT 320
Db        980 CCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAAGCTCAAAATGTTACCAACAT 1039
Qy        321 GCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGAC 380
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Db       1040 ACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTGCATCCCTTTTAC 1099

Qy        381 CGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGC 440

Db       1100 GGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAACACTATGTGTAAACTCACTTC 1159

Qy        441 CTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGA 500

Db       1160 CTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTATTGA 1219

Qy        501 GAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCT 560

Db       1220 ACGATATCAGCTGATTGTGAACCCCCGTGGCTGGAAACCCAGAGTAGCTCATGCCTATTG 1279

Qy        561 GGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAG 620

Db       1280 GGGGATCATCTTGATTTGGCTCATTTCTCTGACATTGTCTATTCCCTTATTCCTGTCCTA 1339

Qy        621 CATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAA 680

Db       1340 CCACCTCACCAATGAGCCCTTTCATAATCTCTCTCTCCCTACTGACATCTACACCCACCA 1399

Qy        681 GGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCT 740

Db       1400 GGTAGCTTGTGTGGAGATTTGGCCTTCTAAACTGAACCAACTCCTCTTTTCTACATCATT 1459

Qy        741 GCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTA 800

Db       1460 ATTTATGCTCCAGTATTTTGTCCCTCTGGGTTTCATTCTTATCTGCTACCTGAAGATCGT 1519

Qy        801 CCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTG---CGAGC 857

Db       1520 TCTCTGCCTCCGAAAAAGAACTAGGCAGGTGGACAGGAGAAAGGAAAATAAGAGCCGTCT 1579

Qy        858 TGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCT 917

Db       1580 CAATGAGAACAAGAGGGTAAATGTGATGTTGATTTCCATCGTAGTGACTTTTGGAGCCTG 1639

Qy        918 CTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCAT 977

Db       1640 CTGGTTGCCCTTGAACATTTTCAATGTCATCTTCGACTGGTATCATGAGATGCTGATGAG 1699

Qy        978 CTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGT 1037

Db       1700 CTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGATTGCTATGGTTTCTACTTGCAT 1759

Qy       1038 CAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGT 1097

Db       1760 AAATCCTCTCTTTTATGGATTTCTCAACAAAAACTTCCAGAAGGATCTAATGATGCTTAT 1819

Qy       1098 GCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGT 1157

Db       1820 TCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTATGAAAATATTGCCATGTCTACTAT 1879

Qy       1158 ACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTA 1214

Db       1880 GCACACAGATGAATCCAAGGGATCATTAAAACTGGCTCACATACCAACAGGCATATA 1936
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RESULT 14
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XX
AC AAI72369;
XX
DT 15-MAY-2002 (first entry)
XX
DE NPY6-R gene.
XX
KW Gene; non-human; transgenic; mouse; G protein-coupled receptor; GPCR;
KW gene therapy; neurological disease; neuropsychological disease; KOR3;
KW psychotic illness; DEZ receptor; CB2R; adrenomedullin receptor; CRFR2;
KW corticotropin-releasing factor receptor; neuropeptide Y receptor gene;
KW N-formylpeptide receptor-like 3; FPRL3; NPY6-R; kappa-3 opiate receptor;
KW metabotropic glutamate receptor; mGluR8; MAS receptor; NPY4-R;
KW targeting arm; ds.
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OS Mus musculus.
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FH Key Location/Qualifiers
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FT /*tag= a
FT /note= "Deleted in targeting construct"
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PN WO200203789-A2.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-US021498.
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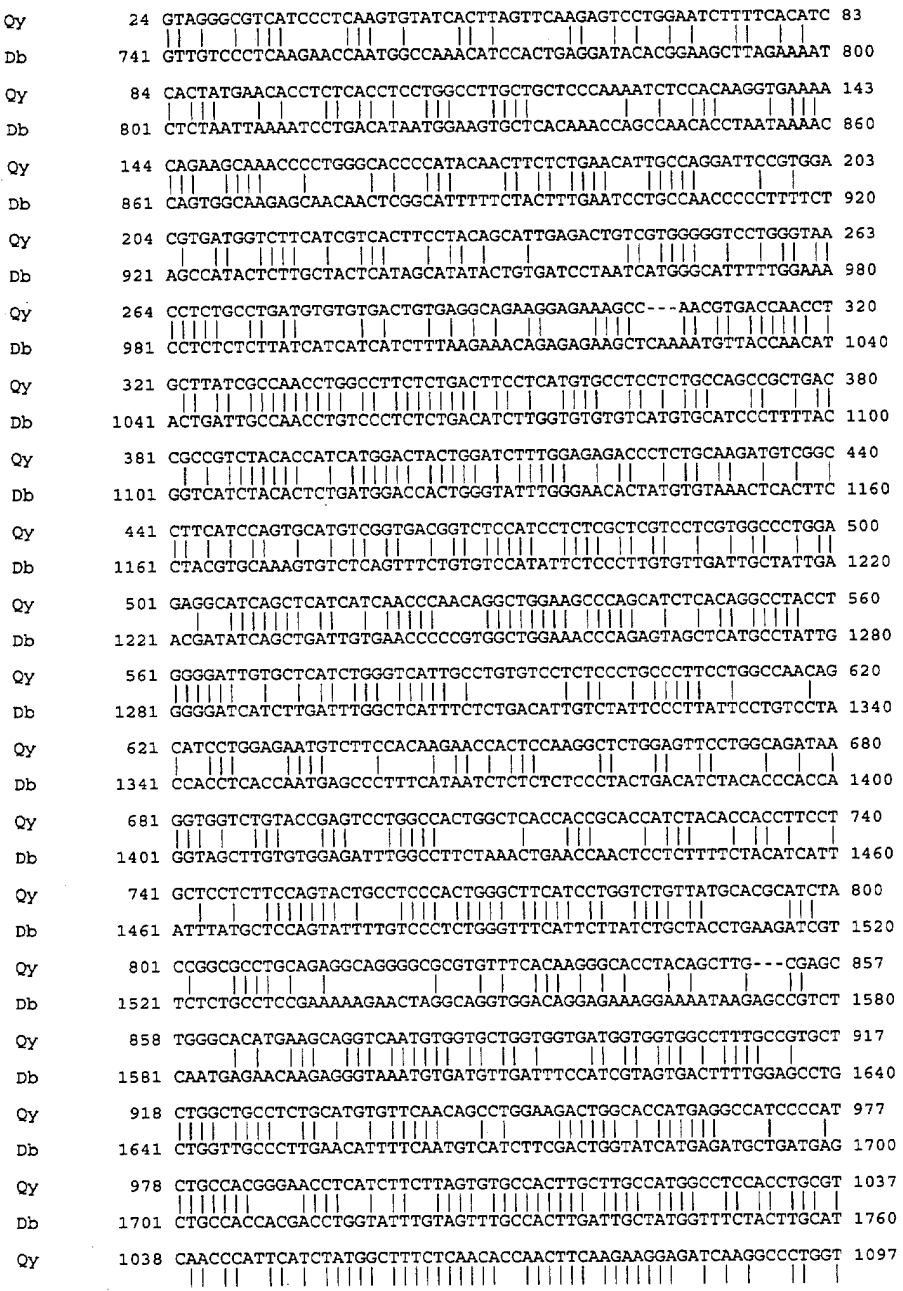
PR 06-JUL-2000; 2000US-0216108P.
PR 06-JUL-2000; 2000US-0216250P.
PR 06-JUL-2000; 2000US-0216252P.
PR 06-JUL-2000; 2000US-0216253P.
PR 06-JUL-2000; 2000US-0216254P.
PR 06-JUL-2000; 2000US-0216259P.
PR 06-JUL-2000; 2000US-0216260P.
PR 06-JUL-2000; 2000US-0216271P.
PR 06-JUL-2000; 2000US-0216473P.
PR 06-JUL-2000; 2000US-0216475P.
PR 19-JUL-2000; 2000US-0219403P.
PR 27-JUL-2000; 2000US-0221473P.
PR 27-JUL-2000; 2000US-0221474P.
PR 27-JUL-2000; 2000US-0221484P.
PR 27-JUL-2000; 2000US-0221490P.
PR 27-JUL-2000; 2000US-0221497P.
PR 07-AUG-2000; 2000US-0223625P.
PR 06-DEC-2000; 2000US-0251815P.
PR 16-JAN-2001; 2001US-0262137P.
PR 16-JAN-2001; 2001US-0262138P.
PR 29-MAR-2001; 2001US-0280264P.
PR 26-JUN-2001; 2001US-0300929P.
XX
PA (DELT-) DELTAGEN INC.
XX
PI Allen KD, Brennan TJ;
XX
DR WPI; 2002-154854/20.
XX
PT Novel non-human transgenic animal, preferably transgenic mice comprising
PT disruptions in target G protein-coupled receptor gene, useful for
PT identifying an agent that modulates expression or function of target
PT gene.
XX
PS Example 7; Fig 19; 93pp; English.
XX
CC This sequence represents the neuropeptide Y receptor gene (NPY6-R). The
CC targeting arms (AAI72370-71) were used to disrupt this gene. The
CC resulting sequence was used in the production of a non-human transgenic
CC animal, preferably a mouse, with targeted G protein-coupled receptor gene
CC disruption in the NPY6-R gene. The transgenic animal is useful for
CC identifying an agent that modulates the expression or function of the
CC target gene, by administering an agent, and determining whether the
CC expression or function of the target is modulated. It is also useful for
CC testing the efficacy of proposed genetic and pharmacological therapies
CC for human genetic diseases, such as neurological, neuropsychological or
CC psychotic illnesses. The transgenic mice are useful as models for
CC diseases, disorders or conditions associated with phenotypes relating to
CC a disruption in a target, and to identify drugs, pharmaceuticals,
CC therapies and interventions which may be effective in treating a disease
CC or other phenotypic characteristics of the animal
XX
SQ Sequence 2281 BP; 695 A; 466 C; 460 G; 659 T; 0 U; 1 Other;

Query Match 21.1%; Score 278.6; DB 6; Length 2281;

Best Local Similarity 53.2%; Pred. No. 1.8e-57;
Matches 637; Conservative 0; Mismatches 554; Indels 6; Gaps 2;



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Qy 1098 GCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGT 1157

Db 1821 TCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTATGAAAATATTGCCATGTCTACTAT 1880

Qy 1158 ACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTA 1214

Db 1881 GCACACAGATGAATCCAAGGGATCATTAAAACTGGCTCACATACCAACAGGCATATA 1937

RESULT 15
AAT36128
ID AAT36128 standard; cDNA; 1499 BP.
XX
AC AAT36128;
XX
DT 25-OCT-1996 (first entry)
XX
DE Human neuropeptide Y Yx receptor cDNA.
XX
KW Neuropeptide Y Yx receptor; NPY Yx; G-protein coupled receptor; obesity;
KW diabetes; cardiac vasospasm; Parkinson's disease; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 182. .1294
FT /*tag= a
XX
PN WO9623809-A1.
XX
PD 08-AUG-1996.
XX
PF 30-JAN-1996; 96WO-US001444.
XX
PR 03-FEB-1995; 95US-00383746.
PR 03-APR-1995; 95US-00415818.
XX
PA (MERI) MERCK & CO INC.
XX
PI Cascieri MA, Linemeyer DL, Macneil DJ, Shiao L, Strader C;
PI Weinberg DH, Tan CP;
XX
DR WPI; 1996-371369/37.
DR P-PSDB; AAW02100.
XX
PT DNA mol. encoding neuro:peptide Y Yx receptor - useful in assays to
PT identify cpds. which bind to receptor, useful to treat, e.g. obesity,
PT diabetes, cardiac vasospasm and Parkinson's disease.
XX
PS Claim 36; Page 53-54; 65pp; English.
XX
CC A cDNA clone (AAT36128) codes for human neuropeptide Y subtype Yx (NPY
CC Yx) receptor (AAW02100). It was obtd. from a human heart cDNA library
CC using a probe obtd. by PCR amplification of human genomic DNA using
CC primers (see also AAT36135-36) based on the mouse NPY Yx receptor
CC (AAT36127). Vectors were constructed to allow expression of the human NPY
CC Yx receptor DNA in mammalian (COS-7) cells. The recombinant receptor, or
CC transformed host cells, can be used to screen for cpds. that modulate the
CC function of the receptor, or modulate the expression of nucleic acids
CC encoding the receptor. Such cpds. are useful for treating a variety of
CC disease conditions
XX
SQ Sequence 1499 BP; 399 A; 400 C; 279 G; 421 T; 0 U; 0 Other;

Query Match 20.2%; Score 266; DB 2; Length 1499;
Best Local Similarity 53.9%; Pred. No. 1.8e-54;
Matches 592; Conservative 0; Mismatches 500; Indels 6; Gaps 2;

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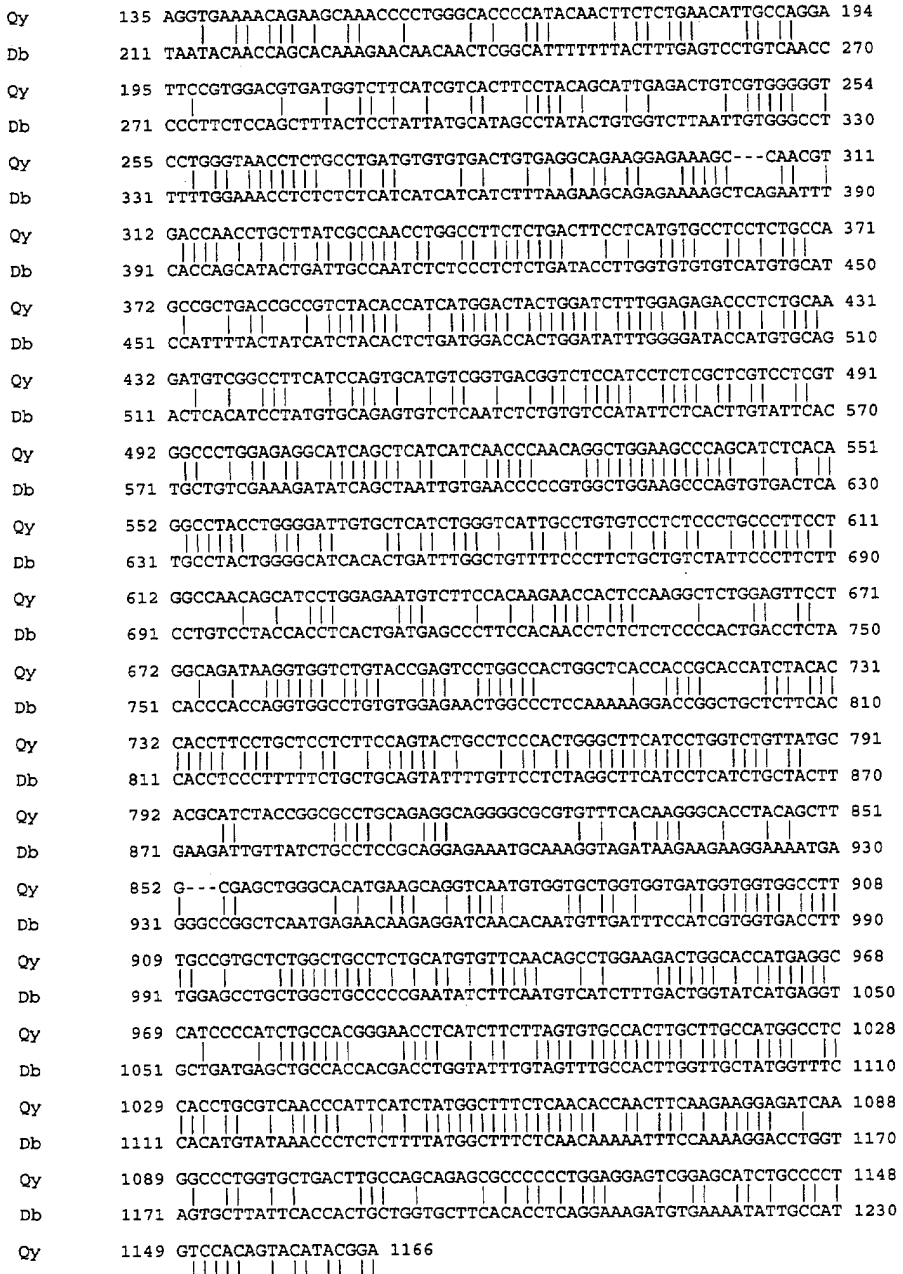

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Job time : 591 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 10:52:27 ; Search time 3773 Seconds
(without alignments)
10447.410 Million cell updates/sec

Title: US-09-430-775-1
Perfect score: 1320
Sequence: 1 AGTATTGTTTGTCTGTTTGC.....CCAGCATTCCTGGCTTTCTG 1320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
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15: em_estfun:*
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17: em_gss_hum:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	797.6	60.4	3628	11	AK035505	AK035505 Mus muscu
c	2	396.6	30.0	426	12	BG875680	BG875680 MR2-CN003
	3	371.2	28.1	602	10	BF040649	BF040649 BP250021A
	4	371.2	28.1	642	10	BF041396	BF041396 BP250008B
c	5	363.8	27.6	453	13	BQ319790	BQ319790 CM0-CT081
c	6	342.8	26.0	406	10	AW378515	AW378515 QV4-HT022
	7	303	23.0	1149	29	AY413582	AY413582 Mus muscu
	8	287.6	21.8	679	13	BY733731	BY733731 BY733731
	9	278.6	21.1	2570	11	AK030279	AK030279 Mus muscu
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	11	254.2	19.3	639	10	BB628025	BB628025 BB628025
	12	252.4	19.1	1152	29	AY413581	AY413581 Pan trogl
	13	185.8	14.1	936	13	BU840743	BU840743 AGENCOURT
	14	159.8	12.1	669	13	BX506438	BX506438 DKFZp779B
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	19	142.2	10.8	621	9	AI790953	AI790953 uk49a05.y
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	23	134.8	10.2	1296	29	AY411593	AY411593 Mus muscu
	24	130	9.8	3336	11	AK018543	AK018543 Mus muscu
c	25	129	9.8	469	28	AQ383893	AQ383893 RPCI11-13
	26	126.6	9.6	1146	29	AY400449	AY400449 Homo sapi
	27	126.4	9.6	524	9	AI908179	AI908179 IL-BT164-
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	29	116.4	8.8	1070	29	CNS03SN1	AL258742 Tetraodon
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	35	104	7.9	2199	11	AK081276	AK081276 Mus muscu
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c	39	92.2	7.0	405	28	AZ237363	AZ237363 RPCI-23-8
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	43	87.6	6.6	2090	11	BC033742	BC033742 Homo sapi
	44	87	6.6	762	14	CD559554	CD559554 AGENCOURT
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ALIGNMENTS

RESULT 1
AK035505
LOCUS AK035505 3628 bp mRNA linear HTC 19-SEP-2003
DEFINITION Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530057L11 product:NEUROPEPTIDE Y RECEPTOR TYPE 4, full insert sequence.
ACCESSION AK035505
VERSION AK035505.1 GI:26330703
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3628)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 60.4%; Score 797.6; DB 11; Length 3628;
Best Local Similarity 76.4%; Pred. No. 8.3e-158;
Matches 993; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

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Qy        18 TGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTT 77
Db       221 TACCTCGCCAGGCTGCATCTCTGAAGTAGGCCCTTTACTCCTGGAGTTCCTGGATCTTCT 280

Qy        78 CACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGG 137
Db       281 CACACCTACCATGAATACCTCTCATTTCTTGGCCCCTCTCTTCCCAGGATCCCTACAGGG 340

Qy       138 TGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTC 197
Db       341 TAAGAATGGGACCAATCCATTGGATTCCCCCTATAATTTCTCTGATGGCTGCCAGGATTC 400

Qy       198 CGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCT 257
Db       401 GGCAGAGCTGTTGGCCTTCATCATCACCACCTACAGCATTGAGACCATCTTGGGGGTCCT 460

Qy       258 GGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAA 317
Db       461 GGGAAACCTCTGCTTGATATTTGTGACCACAAGACAAAAGGAAAAGTCCAATGTGACCAA 520

Qy       318 CCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCT 377
Db       521 CCTGCTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCATCTGCCAACCACT 580

Qy       378 GACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTC 437
Db       581 CACAGTCACCTACACCATCATGGATTACTGGATCTTTGGTGAAGTCCTTTGCAAGATGTT 640

Qy       438 GGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCT 497
Db       641 AACTTTCATCCAGTGTATGTCAGTGACAGTCTCCATCCTCTCACTGGTCCTTGTGGCCCT 700

Qy       498 GGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTA 557
Db       701 GGAGAGGCACCAGCTCATTATCAATCCAACAGGCTGGAAACCCAGTATTTTCCAGGCCTA 760

Qy       558 CCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAA 617
Db       761 CCTGGGGATTGTGGTCATCTGGTTCGTCTCTTGTTTCCTTTCCTTGCCGTTCCTGGCCAA 820

Qy       618 CAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGA 677
Db       821 CAGCACCCTGAATGACCTCTTCCACTACAACCACTCTAAGGTTGTAGAGTTTCTGGAAGA 880

Qy       678 TAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTT 737
Db       881 CAAGGTCGTCTGCTTTGTGTCCTGGTCTTCAGATCACCACCGTCTCATCTATACCACTTT 940

Qy       738 CCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCAT 797
Db       941 TCTGCTGCTCTTTCAGTACTGCATCCCTCTAGCCTTCATCCTGGTCTGCTACATACGCAT 1000

Qy       798 CTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGC 857
Db      1001 CTACCATCGCCTGCAGAGGCAGAAGCATGTGTTCCATGCGCACGCTTGCAGCTCACGAGC 1060
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Qy        858 TGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCT 917
Db       1061 GGGACAGATGAAGCGGATCAACAGCATGCTCATGACAATGGTGACTGCCTTTGCAGTTCT 1120

Qy        918 CTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCAT 977
Db       1121 CTGGCTACCCCTGCATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGC 1180

Qy        978 CTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGT 1037
Db       1181 TTGCCATGGCAACCTCATCTTCTTGATGTGCCACCTGTTGGCCATGGCTTCCACCTGTGT 1240

Qy       1038 CAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGT 1097
Db       1241 CAACCCTTTCATCTATGGCTTTCTCAACATCAACTTCAAGAAGGATATCAAGGCTCTGGT 1300

Qy       1098 GCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGT 1157
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Qy       1218 AGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTAGCTAAGTGGGC 1277
Db       1421 GTGTCTGGGCTTTTCCCTACCATTTT---TTGACACATCCTTTCACTTAGTTAAGAAGAC 1477

Qy       1278 ACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTT 1317
Db       1478 ACATTGCAGGCTGTGATAGCATCCTGTCATTTCTGGCTTT 1517
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RESULT 2
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LOCUS BG875680 426 bp mRNA linear EST 30-MAY-2001
DEFINITION MR2-CN0038-240200-204-g04 CN0038 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG875680
VERSION BG875680.1 GI:14252683
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 426)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR2-CN0038-240200-204-g04&t3=2000-02-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 426.
FEATURES Location/Qualifiers
source 1. .426
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0038"
/note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN

Query Match 30.0%; Score 396.6; DB 12; Length 426;
Best Local Similarity 98.8%; Pred. No. 2.4e-73;
Matches 410; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy        289 AGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGAC 348
Db        426 AGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGAC 367

Qy        349 TTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGG 408
Db        366 TTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGG 307

Qy        409 ATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTC 468
Db        306 ATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTC 247

Qy        469 TCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACA 528
Db        246 TCCATCCTCTCGCTCGACCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACA 187

Qy        529 GGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCC 588
Db        186 GGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCC 127

Qy        589 TGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAAC 648
Db        126 TGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGACTTCCACAAGAAC 67

Qy        649 CACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGC 703
Db         66 CACTCC-AGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGCC 13
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RESULT 3
BF040649
LOCUS BF040649 602 bp mRNA linear EST 10-OCT-2000
DEFINITION BP250021A10G12 Soares normalized bovine placenta Bos taurus cDNA clone BP250021A10G12 5', mRNA sequence.
ACCESSION BF040649
VERSION BF040649.1 GI:10757704
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 602)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

```
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross_match from Washington University Genome Center PHRAP suite.
            This sequence is vector free and at least 200 bp in length.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 602   Std Error: 0.00
            Plate: BP250021A10  row: G  column: 12
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 602.
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                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /clone="BP250021A10G12"
                      /sex="female"
                      /lab_host="DH10B"
                      /clone_lib="Soares normalized bovine placenta"
                      /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                      Site_2: NotI; The cDNA library was contributed by the
                      Soares laboratory and it  was constructed and normalized
                      as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                      M.B. (1996), Genome Research 6(9): 791-806. "
ORIGIN

  Query Match           28.1%;  Score 371.2;  DB 10;  Length 602;
  Best Local Similarity   87.5%;  Pred. No. 6.7e-68;
  Matches  406;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy        155 CCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCT 214
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Db         13 CTCTGTACGCTCCATACAACTTCTCTGACCACTGCCAGGATTCCGTAGACCCCTTGGTCT 72

Qy        215 TCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGA 274
              |||| ||||| |||||||||||||||||  | ||||| |||||||| ||||||||||||
Db         73 TCATTGTCACCTCCTACAGCATTGAGACCATTGTGGGTGTCCTGGGCAACCTCTGCCTGA 132

Qy        275 TGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACC 334
              | ||||||||| | |||||||||||||| ||||| |||||||||||||||||| |||||||
Db        133 TATGTGTGACTATTAGGCAGAAGGAGAAGGCCAATGTGACCAACCTGCTTATTGCCAACC 192

Qy        335 TGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCA 394
              |||||||||||||||||||||||||||||| |||||||||| || || ||  |||||||||
Db        193 TGGCCTTCTCTGACTTCCTCATGTGCCTCATCTGCCAGCCACTCACGGCTATCTACACCA 252

Qy        395 TCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCA 454
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Db        253 TCATGGACTACTGGGTCTTTGGCGAGGTCCTTTGCAAGATATCCACCTTTATCCAGTGCA 312

Qy        455 TGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCA 514
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Db        313 TGTCAGTGACAGTCTCCATCCTCTCGCTTGTCCTTGTGGCTCTGGAGAGGCATCAGCTCA 372

Qy        515 TCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCA 574
              ||| ||| |||||||||||||| |||||  || | |||||||||||||||||||| |||
Db        373 TCACCAATCCAACAGGCTGGAAACCCAGTGTCACCCAGGCCTACCTGGGGATTGTGGTCA 432

Qy        575 TCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAAC 618
              ||||| ||||||| ||  |||||||||||| ||||||||||||
Db        433 TCTGGCTCATTGCTTGCTTCCTCTCCCTGCCGTTCCTGGCCAAC 476


RESULT 4
BF041396
LOCUS       BF041396                642 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  BP250008B10E9 Soares normalized bovine placenta Bos taurus cDNA
            clone BP250008B10E9 5', mRNA sequence.
ACCESSION   BF041396
VERSION     BF041396.1  GI:10758451
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
            Larson,J.H.
  TITLE     Bovine ESTs
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross_match from Washington University Genome Center PHRAP suite.
            This sequence is vector free and at least 200 bp in length. REPEAT
            IN THE SEQUENCE Simple_repeat STRAND (+) ELEMENT (A)n LOCATION
            [621,642].
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 642   Std Error: 0.00
            Plate: BP250008B10  row: E  column: 9
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 642.
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     source           1. .642
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                      /mol_type="mRNA"
                      /db_xref="taxon:9913"
                      /clone="BP250008B10E9"
                      /sex="female"
                      /lab_host="DH10B"
                      /clone_lib="Soares normalized bovine placenta"
                      /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                      Site_2: NotI; The cDNA library was contributed by the
                      Soares laboratory and it  was constructed and normalized
                      as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                      M.B. (1996), Genome Research 6(9): 791-806. "
ORIGIN

  Query Match           28.1%;  Score 371.2;  DB 10;  Length 642;
  Best Local Similarity   87.5%;  Pred. No. 6.9e-68;
  Matches  406;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy        155 CCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCT 214
              | |||  | | |||||||||||||||||| || ||||||||||||| |||    ||||||
Db         13 CTCTGTACGCTCCATACAACTTCTCTGACCACTGCCAGGATTCCGTAGACCCCTTGGTCT 72

Qy        215 TCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGA 274
              |||| ||||| |||||||||||||||||  | ||||| |||||||| ||||||||||||
Db         73 TCATTGTCACCTCCTACAGCATTGAGACCATTGTGGGTGTCCTGGGCAACCTCTGCCTGA 132

Qy        275 TGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACC 334
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Db        133 TATGTGTGACTATTAGGCAGAAGGAGAAGGCCAATGTGACCAACCTGCTTATTGCCAACC 192

Qy        335 TGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCA 394
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Db        193 TGGCCTTCTCTGACTTCCTCATGTGCCTCATCTGCCAGCCACTCACGGCTATCTACACCA 252

Qy        395 TCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCA 454
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Db        253 TCATGGACTACTGGGTCTTTGGCGAGGTCCTTTGCAAGATATCCACCTTTATCCAGTGCA 312
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Qy        455 TGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCA 514
              |||| ||||| |||||||||||||||||| ||||| ||||| ||||||||||||||||||
Db        313 TGTCAGTGACAGTCTCCATCCTCTCGCTTGTCCTTGTGGCTCTGGAGAGGCATCAGCTCA 372

Qy        515 TCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCA 574
              ||| ||| |||||||||||||| ||||| || | |||||||||||||||||||||| |||
Db        373 TCACCAATCCAACAGGCTGGAAACCCAGTGTCACCCAGGCCTACCTGGGGATTGTGGTCA 432

Qy        575 TCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAAC 618
              ||||| ||||||| ||  |||||||||||| ||||||||||||
Db        433 TCTGGCTCATTGCTTGCTTCCTCTCCCTGCCGTTCCTGGCCAAC 476


RESULT 5
BQ319790/c
LOCUS       BQ319790                453 bp    mRNA    linear   EST 17-MAY-2002
DEFINITION  CM0-CT0811-200401-823-d10 CT0811 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ319790
VERSION     BQ319790.1  GI:20926238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-CT0811-
            200401-823-d10&t3=2001-04-20&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 42
            High quality sequence stop: 78.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CT0811"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

  Query Match             27.6%;  Score 363.8;  DB 13;  Length 453;
  Best Local Similarity   95.1%;  Pred. No. 2.2e-66;
  Matches  408;  Conservative    0;  Mismatches   17;  Indels    4;  Gaps    3;

Qy        337 GCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATC 396
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Db        452 GCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCTCCGTGTACACCATC 393

Qy        397 ATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATG 456
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        392 ATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTTATCCAGTGCATG 333

Qy        457 TCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATC 516
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Db        332 TCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATC 273

Qy        517 -ATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCAT 575
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        272 TATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTTAT 213

Qy        576 CTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGT 635
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        212 CTGGGTCATTGCCTGTGTCCTCTACCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGT 153

Qy        636 CTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGA 695
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        152 CTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGA 93

Qy        696 GTCCTGGCCACTGGCTC--ACCACCGCACCATCTACACCACCTTCCTGCTCCT-CTTCCA 752
              |||||| || || ||||    ||| |||| || |||||||||||| |||||||  || ||
Db         92 GTCCTGTCCCCTCGCTCTTCACACAGCACGATATACACCACCTTCTTGCTCCTGGTTACA 33

Qy        753 GTACTGCCT 761
              |||||||||
Db         32 GTACTGCCT 24


RESULT 6
AW378515/c
LOCUS       AW378515                406 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  QV4-HT0222-091199-024-f01 HT0222 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW378515
VERSION     AW378515.1  GI:6883174
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 406)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-HT0222-
            091199-024-f01&t3=1999-11-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 10
            High quality sequence stop: 405.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0222"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
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               profiles into  the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
ORIGIN

  Query Match             26.0%;  Score 342.8;  DB 10;  Length 406;
  Best Local Similarity   98.5%;  Pred. No. 5.8e-62;
  Matches  388;  Conservative    0;  Mismatches    2;  Indels    4;  Gaps    4;

Qy        499 GAGAGGCATCAGCTCATCATCAACCCAACAGG-CTGGAAGCCCAGCATCTCACAGGCCTA 557
Db        406 GAGAGGCATCAGCTCATCATCAACCCAACAGGCCTGGAAGCCCAGCATCTCACAGGCCTA 347

Qy        558 C-CTGGGGATTGTGCTCATCTGGGTCATTGCC-TGTGTCCTCTCCCTGCCCTTCCTGGCC 615
Db        346 CACTGGGGATTGTGCTCATCTGGGTCATTGCCATGTGTCCTCTCCCTGCCCTTCCTGGCC 287

Qy        616 AACAGCATCCTGGAGAATGTCTTCCACAAGAACCA-CTCCAAGGCTCTGGAGTTCCTGGC 674
Db        286 AACAGCATCCTGGAGAATGTCTTCCACAAGAACCACCTCCAAGGCTCTGGAGTTCCTGGC 227

Qy        675 AGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCAC 734
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Qy        735 CTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACG 794
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Qy        795 CATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCG 854
Db        106 CATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCG 47

Qy        855 AGCTGGGCACATGAAGCAGGTCAATGTGGTGCTG 888
Db         46 AGCTGGGCACATGAAGCAGGTCAATGTGGTGCTG 13


RESULT 7
AY413582
LOCUS       AY413582                1149 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus NPY1R gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY413582
VERSION     AY413582.1  GI:39769544
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1149)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1149)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1149
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ORIGIN

  Query Match             23.0%;  Score 303;  DB 29;  Length 1149;
  Best Local Similarity   57.7%;  Pred. No. 2.4e-53;
  Matches  584;  Conservative    0;  Mismatches  420;  Indels    9;  Gaps    2;

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Db         87 TGATGACTGCCACCTGCCCTTGGCTGTGATATTCACCTTGGCTCTCGCTTATGGGGCGGT 146

Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
Db        147 GATTATTCTTGGCGTCTCTGGAAACCTGGCATTGATCATAATCATTCTGAAACAGAAGGA 206

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
Db        207 GATGAGAAATGTCACCAACATTCTGATCGTGAACCTCTCCTTCTCAGACTTGCTCGTTGC 266

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
Db        267 GGTCATGTGTCTCCCGTTCACTTTTGTATATACACTGATGGACCACTGGGTCTTCGGGGA 326

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
Db        327 GACCATGTGCAAACTGAATCCCTTTGTACAGTGTGTCTCCATCACAGTATCCATTTTCTC 386

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db        387 GCTGGTTCTCATCGCTGTGGAACGGCATCAGCTAATCATCAACCCAAGAGGGTGGAGACC 446

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db        447 AAACAATAGACATGCTTACATAGGCATTACTGTCATTTGGGTCCTTGCAGTGGCTTCTTC 506

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
Db        507 TCTGCCCTTTGTGATCTATCAAATTCTGACCGACGAGCCCTTCCAAAA------TGTGTC 560

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719
Db        561 ACTTGCGGCGTTCAAGGACAAGTATGTGTGCTTTGACAAATTCCCATCTGACTCTCACAG 620

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
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Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGG 839
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Qy        840 CACCTACAG---CTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896
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Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
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Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
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Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
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Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
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RESULT 8
BY733731
LOCUS BY733731 679 bp mRNA linear EST 17-DEC-2002
DEFINITION BY733731 RIKEN full-length enriched, adult male gall bladder Mus musculus cDNA clone G630073I24 5', mRNA sequence.
ACCESSION BY733731
VERSION BY733731.1 GI:27146858
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 679)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .679
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="G630073I24"
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ORIGIN

Query Match 21.8%; Score 287.6; DB 13; Length 679;
Best Local Similarity 74.5%; Pred. No. 3.5e-50;
Matches 359; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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Db        198 TACCTCGCCAGGCTGCATCTCTGAAGTAGGCCCTTTACTCCTGGAGTTCCTGGATCTTCT 257

Qy         78 CACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGG 137
              |||| | || ||||| ||||||||  || |||||   ||  |||||  ||| | ||| ||
Db        258 CACACCTACCATGAATACCTCTCATTTCTTGGCCCCTCTCTTCCCAGGATCCCTACAGGG 317

Qy        138 TGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTC 197
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Db        318 TAAGAATGGGACCAATCCATTGGATTCCCCCTATAATTTCTCTGATGGCTGCCAGGATTC 377

Qy        198 CGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCT 257
              |  ||  || ||| |||||||| |||  |||||||||||||||||  || ||||||||||
Db        378 GGCAGAGCTGTTGGCCTTCATCATCACCACCTACAGCATTGAGACCATCTTGGGGGTCCT 437

Qy        258 GGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAA 317
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Db        438 GGGAAACCTCTGCTTGATATTTGTGACCACAAGACANAAGGAAAAGTCCAATGTGACCAA 497

Qy        318 CCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCT 377
              ||| || || ||||||||||||||||||||||||||||||||||||| ||||||| || ||
Db        498 CCTACTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCATCTGCCAACCACT 557

Qy        378 GACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTC 437
              || | |  |||||||||||||| ||||||||||||| || | |  |  ||||||
Db        558 CACAGTCACCTACACCATCATGGATTACTGGATCTTTGGTGAAAGTCCTTTGCAGATGTT 617

Qy        438 GGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCT 497
                |  |||| ||||| ||||| ||||| |||  ||||||||| || ||||| |||| |||
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Qy        498 GG 499
              ||
Db        678 GG 679
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RESULT 9
AK030279
LOCUS AK030279 2570 bp mRNA linear HTC 18-SEP-2003
DEFINITION Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031404D23

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            product:NEUROPEPTIDE Y RECEPTOR TYPE 6, full insert sequence.
ACCESSION   AK030279
VERSION     AK030279.1  GI:26326262
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2570)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES                Location/Qualifiers
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                        /sex="female"
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                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="11 days pregnant adult"
     CDS                383. .1498
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                        100%length, match=1113)
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                        /codon_start=1
                        /protein_id="BAC26875.1"
                        /db_xref="GI:26326263"
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                        VFGNTMCKLTSYVQSVSVSVSIFSLVLIAIERYQLIVNPRGWKPRVAHAYWGIILIWL
                        ISLTLSIPLFLSYHLTNEPFHNLSLPTDIYTHQVACVEIWPSKLNQLLFSTSLFMLQY
                        FVPLGFILICYLKIVLCLRKRTRQVDRRKENKSRLNENKRVNVMLISIVVTFGACWLP
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ORIGIN
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Query Match 21.1%; Score 278.6; DB 11; Length 2570;
Best Local Similarity 53.2%; Pred. No. 5.1e-48;
Matches 637; Conservative 0; Mismatches 554; Indels 6; Gaps 2;

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Qy         24 GTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTTCACATC 83
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Db        301 GTTGTCCCTCAAGAACCAATGGCCAAACATCCACTGAGGATACACGGAAGCTTAGAAAAT 360

Qy         84 CACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAA 143
              | |||   | |   || || |  |||   ||||         |  |  |||   | |||
Db        361 CTCTAATTAAAATCCTGACATAATGGAAGTGCTCACAAACCAGCCAACACCTAATAAAAC 420

Qy        144 CAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGA 203
              |||  ||||   |      | |  |||    || || ||||  |||||     |  |
Db        421 CAGTGGCAAGAGCAACAACTCGGCATTTTTCTACTTTGAATCCTGCCAACCCCCTTTTCT 480

Qy        204 CGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAA 263
              |  ||  ||||  |  |||   | || |   |       || ||||  |  | || ||
Db        481 AGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTAATCATGGGCATTTTTGGAAA 540

Qy        264 CCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCC---AACGTGACCAACCT 320
              |||||  || ||     | |  | | | |  ||    ||||    || || ||||||  |
Db        541 CCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAAGCTCAAAATGTTACCAACAT 600

Qy        321 GCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGAC 380
              || || ||||||||| || |||||||| || |  ||||  || | |||   ||  | ||
Db        601 ACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTGCATCCCTTTTAC 660

Qy        381 CGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGC 440
              | | |||||||  | ||||| ||||| | |||||  | ||  | || ||  |  | |
Db        661 GGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAACACTATGTGTAAACTCACTTC 720

Qy        441 CTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGA 500
              || | ||  |  | || ||  | || |||||  |||| || ||  |  | ||  | ||
Db        721 CTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTATTGA 780

Qy        501 GAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCT 560
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Db        781 ACGATATCAGCTGATTGTGAACCCCCGTGGCTGGAAACCCAGAGTAGCTCATGCCTATTG 840

Qy        561 GGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAG 620

Db        841 GGGGATCATCTTGATTTGGCTCATTTCTCTGACATTGTCTATTCCCTTATTCCTGTCCTA 900

Qy        621 CATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAA 680

Db        901 CCACCTCACCAATGAGCCCTTTCATAATCTCTCTCCCTACTGACATCTACACCCACCA 960

Qy        681 GGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCT 740

Db        961 GGTAGCTTGTGTGGAGATTTGGCCTTCTAAACTGAACCAACTCCTCTTTTCTACATCATT 1020

Qy        741 GCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTA 800

Db       1021 ATTTATGCTCCAGTATTTTGTCCCTCTGGGTTTCATTCTTATCTGCTACCTGAAGATCGT 1080

Qy        801 CCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTG---CGAGC 857

Db       1081 TCTCTGCCTCCGAAAAAGAACTAGGCAGGTGGACAGGAGAAAGGAAAATAAGAGCCGTCT 1140

Qy        858 TGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCT 917

Db       1141 CAATGAGAACAAGAGGGTAAATGTGATGTTGATTTCCATCGTAGTGACTTTTGGAGCCTG 1200

Qy        918 CTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCAT 977

Db       1201 CTGGTTGCCCTTGAACATTTTCAATGTCATCTTCGACTGGTATCATGAGATGCTGATGAG 1260

Qy        978 CTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGT 1037

Db       1261 CTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGATTGCTATGGTTTCTACTTGCAT 1320

Qy       1038 CAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGT 1097

Db       1321 AAATCCTCTCTTTTATGGATTTCTCAACAAAAACTTCCAGAAGGATCTAATGATGCTTAT 1380

Qy       1098 GCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGT 1157

Db       1381 TCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTATGAAAATATTGCCATGTCTACTAT 1440

Qy       1158 ACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTA 1214

Db       1441 GCACACAGATGAATCCAAGGGATCATTAAAACTGGCTCACATACCAACAGGCATATA 1497
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RESULT 10
AY413580
LOCUS AY413580 1155 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens NPY1R gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY413580
VERSION AY413580.1 GI:39769542
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1155)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1155)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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gene <1. .>1155
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/locus_tag="HCM4938"
ORIGIN

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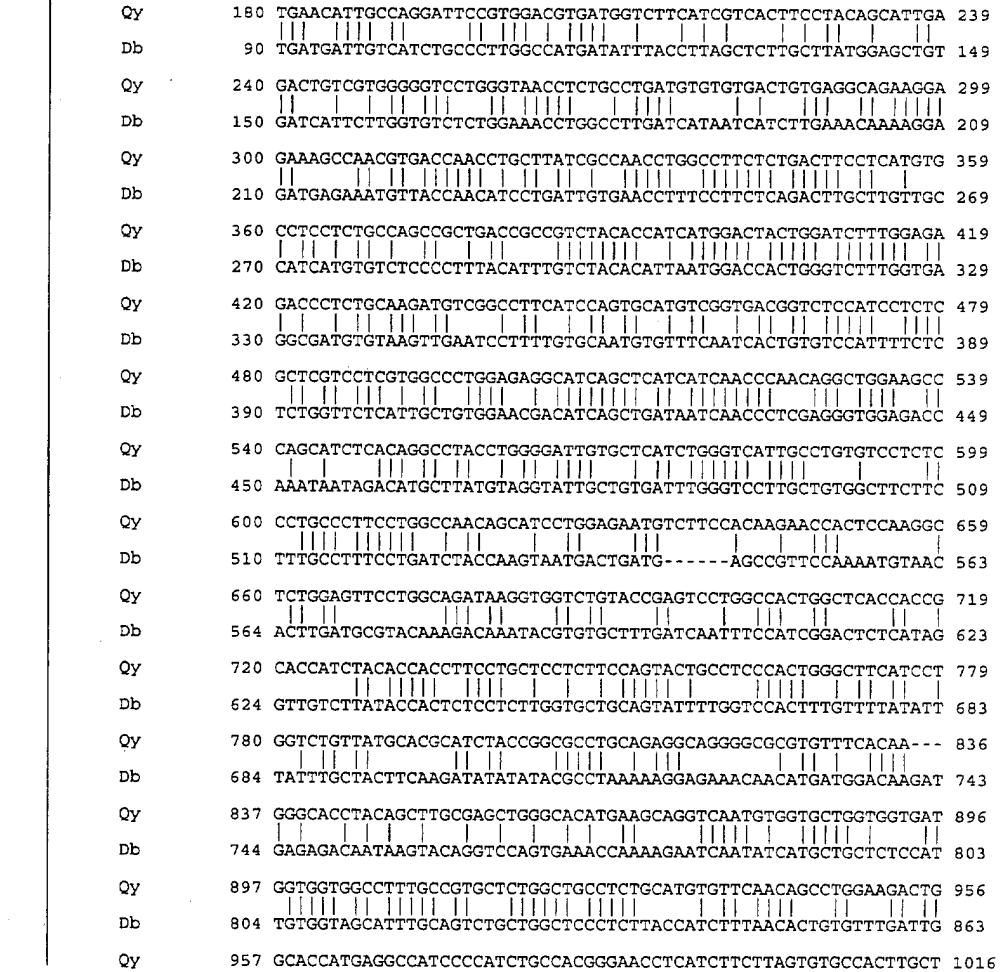
Best Local Similarity 55.0%; Pred. No. 1e-43;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;



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Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299

Db        150 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 209

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359

Db        210 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 269

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419

Db        270 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 329

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479

Db        330 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 389

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539

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Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599

Db        450 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 509

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659

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Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719

Db        564 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 623

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779

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Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836

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Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896

Db        744 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 803

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956

Db        804 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 863

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
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Db        864 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 923

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076

Db        924 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 983

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136

Db        984 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1043

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196

Db       1044 AACAATAGCCATGTCCACGATGCACACAGATGTTTCCAAAACTTCTTTGAAGCAA----G 1099

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224

Db       1100 CAAGCCCAGTCGCATTTAAAAAAATCAA 1127


RESULT 11
BB628025
LOCUS       BB628025                639 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB628025 RIKEN full-length enriched, adult male urinary bladder Mus
            musculus cDNA clone 9530057L11 5', mRNA sequence.
ACCESSION   BB628025
VERSION     BB628025.1  GI:16465558
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .639
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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                     /clone_lib="RIKEN full-length enriched, adult male urinary
                     bladder"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 370.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from
                     Lambda FLC I."
ORIGIN

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  Best Local Similarity   75.4%;  Pred. No. 4e-43;
  Matches  316;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy         18 TGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTT 77

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Qy         78 CACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGG 137

Db        281 CACACCTACCATGAATACCTCTCATTTCTTGGCCCCTCTCTTCCCAGGATCCCTACAGGG 340

Qy        138 TGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTC 197

Db        341 TAAGAATGGGACCAATCCATTGGATTCCCCCTATAATTTCTCTGATGGCTGCCAGGATTC 400

Qy        198 CGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCT 257

Db        401 GGCAGAGCTGTTGGCCTTCATCATCACCACCTACAGCATTGAGACCATCTTGGGGGTCCT 460

Qy        258 GGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAA 317

Db        461 GGGAAACCTCTGCTTGATATTTGTGACCACAAGACAAAAGGAAAAGTCCAATGTGACCAA 520

Qy        318 CCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCT 377

Db        521 CCTGCTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCATCTGCCAACCACT 580

Qy        378 GACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGT 436

Db        581 CACAGTCACCTACACCATCATGGATTACTGGATCTTTGGTGAAGTCCTTTGCAAGATGT 639


RESULT 12
AY413581
LOCUS       AY413581                1152 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Pan troglodytes NPY1R gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY413581
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VERSION     AY413581.1  GI:39769543
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1152)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1152)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN

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  Matches  566;  Conservative    0;  Mismatches  469;  Indels   13;  Gaps    3;

Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239
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Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
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Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
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Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
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Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
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Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db        390 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCTCGAGGGTGGAGACC 449

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db        450 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 509

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
Db        510 TTTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCATTCCAAAATGTAAC 563

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719
Db        564 ACTTGATGCATACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 623

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
Db        624 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTGGTCCACTTTGTTTTATATT 683

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836
Db        684 TATTTGCTACTTCAAGATATATATACGCCTAAAAAGGAGAAACAACATGATGGACAAGAT 743

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896
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Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
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Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
Db        864 GAATCATCAGATCATTGCCACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 923

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
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Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
Db        984 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1043

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db       1044 AACAATAGCCATGTCCACCATGCACACAGATGTTTCCAAAACTTCTTTGAAGCAA----G 1099

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224
Db       1100 CAAGCCCAGTCGCATTTAAAAAAATCAA 1127


RESULT 13
BU840743
LOCUS       BU840743                 936 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_8967758 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6490858
            5', mRNA sequence.
ACCESSION   BU840743
VERSION     BU840743.1  GI:24025143
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 936)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14041  row: f  column: 11
            High quality sequence stop: 582.
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                  Average insert size 3.3 kb. Library enriched for
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                  Note: this is a NIH_MGC Library."
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  Matches  379;  Conservative    0;  Mismatches  277;  Indels    7;  Gaps    2;

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Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
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Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGG 839
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DEFINITION  DKFZp779B1117_r1 779 (synonym: hnccl) Homo sapiens cDNA clone
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ACCESSION   BX506438
VERSION     BX506438.1  GI:32046673
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 669)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
            Wellenreuther,R., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp779B1117) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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ORIGIN

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Qy        347 ACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACT 406
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Qy        527 CAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTG 586
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Qy        767 TGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCG 826
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ACCESSION AY420480
VERSION AY420480.1 GI:39776437
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1113)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1113)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
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Matches 462; Conservative 0; Mismatches 420; Indels 24; Gaps 3;

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GenCore version 5.1.6

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1320	100.0	1320	2	US-08-555-268A-1	Sequence 1, Appli
3	1320	100.0	1320	2	US-08-495-695B-1	Sequence 1, Appli
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15	257.6	19.5	1152	3	US-09-045-186-3	Sequence 3, Appli
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31	156	11.8	1331	3	US-08-513-974B-322	Sequence 322, App
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ALIGNMENTS

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; Sequence 1, Application US/08176412
; Patent No. 5516653
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,412
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743/JPW/TEP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
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;      NAME/KEY:  CDS
;      LOCATION:  88..1212
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Db        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720

Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140

Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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Db       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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RESULT 2
US-08-555-268A-1
; Sequence 1, Application US/08555268A
; Patent No. 5958709
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/555,268A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-Z/JPW/MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0526
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  88..1212
US-08-555-268A-1

  Query Match           100.0%;  Score 1320;  DB 2;  Length 1320;
  Best Local Similarity  100.0%;  Pred. No. 0;
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  Matches 1320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
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Db          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
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Db         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120

Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180

Qy        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
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Db        181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240

Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300

Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
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Db        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360

Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420

Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
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Db        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480

Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
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Db        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540

Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
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Db        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600

Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
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Db        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660

Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
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Db        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720

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Db        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780

Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
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Db        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840

Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
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Db        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
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Db        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
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Db       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080

Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
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Db       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140

Qy       1141 CTGCCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
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Db       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200

Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
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Db       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260

Qy       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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Db       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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RESULT 3
US-08-495-695B-1
; Sequence 1, Application US/08495695B
; Patent No. 5976814
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/495,695B
;      FILING DATE:  13-Jan-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-A-PCT-US/JPW/JHB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  88..1212
US-08-495-695B-1

  Query Match           100.0%;  Score 1320;  DB 2;  Length 1320;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840

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Db       1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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RESULT 4
PCT-US94-14436-1
; Sequence 1, Application PC/TUS9414436
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14436
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-A-PCT\JPW\MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  88..1212
PCT-US94-14436-1

  Query Match             100.0%;  Score 1320;  DB 5;  Length 1320;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1320;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60

Db          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60

Qy         61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
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Db        61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
Qy       121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
Db       121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
Qy       181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
Db       181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
Qy       241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
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Qy       301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
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Qy       361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
Db       361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
Qy       421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
Db       421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
Qy       481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
Db       481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
Qy       541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
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Qy       601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
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Qy       661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
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Qy       721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
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Qy       781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
Db       781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
Qy       841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
Db       841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
Qy       901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
Db       901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
Qy       961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
Db       961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
Qy      1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
Db      1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
Qy      1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
Db      1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
Qy      1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
Db      1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
Qy      1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
Db      1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTC 1260
Qy      1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
Db      1261 CACTTAGCTAAGTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTTCTG 1320
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RESULT 5
US-09-016-434-1061
; Sequence 1061, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1061:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1180 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1063629
US-09-016-434-1061

  Query Match             89.4%;  Score 1180;  DB 4;  Length 1180;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-287;
  Matches 1180;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          61 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC 60

Qy         121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 120

Qy         181 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 240
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Db        121 GAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAG 180
Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
Db        181 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 240
Qy        301 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 360
Db        241 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGC 300
Qy        361 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 420
Db        301 CTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAG 360
Qy        421 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 480
Db        361 ACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCG 420
Qy        481 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 540
Db        421 CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCC 480
Qy        541 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 600
Db        481 AGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCC 540
Qy        601 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 660
Db        541 CTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCT 600
Qy        661 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 720
Db        601 CTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGC 660
Qy        721 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 780
Db        661 ACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTG 720
Qy        781 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 840
Db        721 GTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGC 780
Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
Db        781 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 840
Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
Db        841 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 900
Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
Db        901 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 960
Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
Db        961 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1020
Qy       1081 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1140
Db       1021 GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCAT 1080
Qy       1141 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1200
Db       1081 CTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG 1140
Qy       1201 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1240
Db       1141 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCA 1180

RESULT 6
US-08-495-695B-27
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; Sequence 27, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
;   APPLICANT:  Bard, Jonathan A.
;   APPLICANT:  Walker, Mary
;   APPLICANT:  Branchek, Theresa
;   APPLICANT:  Weinshank, Richard L.
;   TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;   TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;   TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;   NUMBER OF SEQUENCES:  33
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Cooper & Dunham
;     STREET:  1185 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  U.S.A.
;     ZIP:  10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.24
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/495,695B
;     FILING DATE:  13-Jan-1997
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  White, John P.
;     REGISTRATION NUMBER:  28,678
;     REFERENCE/DOCKET NUMBER:  44743-A-PCT-US/JPW/JHB
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 278-0400
;     TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  27:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  1439 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  178..1306
US-08-495-695B-27

  Query Match             61.4%;  Score 810.8;  DB 2;  Length 1439;
  Best Local Similarity   78.7%;  Pred. No. 1.3e-194;
  Matches  981;  Conservative    0;  Mismatches  262;  Indels    3;  Gaps    1;

Qy         72 TCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCC 131
Db        162 TCTTCTCACACCCACCATGAATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCCT 221
Qy        132 ACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCA 191
Db        222 ACAAGGTAAGAATGGGACCAACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCA 281
Qy        192 GGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGG 251
Db        282 GGATTCGGCAGATCTGTTGGCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGG 341
Qy        252 GGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGT 311
Db        342 GGTCCTAGGAAACCTCTGCTTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGT 401
Qy        312 GACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCA 371
Db        402 GACCAACCTACTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCA 461
Qy        372 GCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAA 431
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Db        462 GCCGCTCACGGTCACCTACACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAA 521

Qy        432 GATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGT 491

Db        522 GATGTTAACGTTCATCCAGTGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGT 581

Qy        492 GGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACA 551

Db        582 GGCCCTGGAGAGGCACCAGCTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCCA 641

Qy        552 GGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCT 611

Db        642 GGCCTACCTGGGGATTGTGGTCATCTGGTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCT 701

Qy        612 GGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCT 671

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Qy        672 GGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACAC 731

Db        762 GGAAGACAAGGTTGTCTGCTTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACAC 821

Qy        732 CACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGC 791

Db        822 CACCTTTCTGCTGCTCTTCCAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACAT 881

Qy        792 ACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTT 851

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Qy        852 GCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGC 911

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Qy        912 CGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCAT 971

Db       1002 AGTTCTCTGGCTGCCCCTGCATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCAT 1061

Qy        972 CCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCAC 1031

Db       1062 CCCTGCTTGCCATGGCAACCTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCAC 1121

Qy       1032 CTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGC 1091

Db       1122 CTGTGTCAACCCTTTCATCTATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGC 1181

Qy       1092 CCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTC 1151

Db       1182 TCTGGTTCTGACCTGCCGTTGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTC 1241

Qy       1152 CACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCAT 1211

Db       1242 CACTGTGCACACGGACCTCTCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCAT 1301

Qy       1212 TTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTAGCTAA 1271

Db       1302 GTAGTCATGTCTAGGCTCT---TCCGCCATTTCTTTCGACACACCCTTTCACTGAGCTAA 1358

Qy       1272 GTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTT 1317

Db       1359 GTAGACACAATGCAAGCTGTGGTATCATCCTGCCATTTCTGGTCTT 1404


RESULT 7
PCT-US94-14436-27
; Sequence 27, Application PC/TUS9414436
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14436
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-A-PCT\JPW\MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1439 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  178..1306
PCT-US94-14436-27

  Query Match             61.4%;  Score 810.8;  DB 5;  Length 1439;
  Best Local Similarity   78.7%;  Pred. No. 1.3e-194;
  Matches  981;  Conservative    0;  Mismatches  262;  Indels    3;  Gaps    1;

Qy         72 TCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCC 131

Db        162 TCTTCTCACACCCACCATGAATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTCCT 221

Qy        132 ACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCA 191

Db        222 ACAAGGTAAGAATGGGACCAACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCA 281

Qy        192 GGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGG 251

Db        282 GGATTCGGCAGATCTGTTGGCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGG 341

Qy        252 GGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGT 311

Db        342 GGTCCTAGGAAACCTCTGCTTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGT 401

Qy        312 GACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCA 371

Db        402 GACCAACCTACTCATTGCCAACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCA 461

Qy        372 GCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAA 431

Db        462 GCCGCTCACGGTCACCTACACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAA 521

Qy        432 GATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGT 491

Db        522 GATGTTAACGTTCATCCAGTGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGT 581

Qy        492 GGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACA 551
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Db        582 GGCCCTGGAGAGGCACCAGCTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCCA 641

Qy        552 GGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCT 611

Db        642 GGCCTACCTGGGGATTGTGGTCATCTGGTTCATTTCTTGTTTCCTCTCCTTGCCCTTCCT 701

Qy        612 GGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCT 671

Db        702 GGCCAATAGCATCCTGAACGACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCT 761

Qy        672 GGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACAC 731

Db        762 GGAAGACAAGGTTGTCTGCTTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACAC 821

Qy        732 CACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGC 791

Db        822 CACCTTTCTGCTGCTCTTCCAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACAT 881

Qy        792 ACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTT 851

Db        882 GCGTATCTATCAGCGCCTGCAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTC 941

Qy        852 GCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGC 911

Db        942 ACGAGTGGGGCAGATGAAGCGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGC 1001

Qy        912 CGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCAT 971

Db       1002 AGTTCTCTGGCTGCCCCTGCATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCAT 1061

Qy        972 CCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCAC 1031

Db       1062 CCCTGCTTGCCATGGCAACCTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCAC 1121

Qy       1032 CTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGC 1091

Db       1122 CTGTGTCAACCCTTTCATCTATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGC 1181

Qy       1092 CCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTC 1151

Db       1182 TCTGGTTCTGACCTGCCGTTGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTC 1241

Qy       1152 CACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCAT 1211

Db       1242 CACTGTGCACACGGACCTCTCCAAGGGATCTATGAGGATGGGTAGCAAGTCTAACGTCAT 1301

Qy       1212 TTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGCTCTTCCACTTAGCTAA 1271

Db       1302 GTAGTCATGTCTAGGCTCT---TCCGCCATTTCTTTCGACACACCCTTTCACTGAGCTAA 1358

Qy       1272 GTGGGCACACTGCAAGCTGGGGTGGCACCCCAGCATTCCTGGCTTT 1317

Db       1359 GTAGACACAATGCAAGCTGTGGTATCATCCTGCCATTTCTGGTCTT 1404


RESULT 8
US-08-415-818-5
; Sequence 5, Application US/08415818
; Patent No. 5621079
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/415,818
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  822..1937
US-08-415-818-5

  Query Match             21.1%;  Score 278.6;  DB 1;  Length 2280;
  Best Local Similarity   53.2%;  Pred. No. 1.4e-60;
  Matches  637;  Conservative    0;  Mismatches  554;  Indels    6;  Gaps    2;

Qy         24 GTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTTCACATC 83

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Qy         84 CACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAA 143

Db        800 CTCTAATTAAAATCCTGACATAATGGAAGTGCTCACAAACCAGCCAACACCTAATAAAAC 859

Qy        144 CAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGA 203

Db        860 CAGTGGCAAGAGCAACAACTCGGCATTTTTCTACTTTGAATCCTGCCAACCCCCTTTTCT 919

Qy        204 CGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAA 263

Db        920 AGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTAATCATGGGCATTTTTGGAAA 979

Qy        264 CCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCC---AACGTGACCAACCT 320

Db        980 CCTCTCTCTTATCATCATCTTTAAGAAACAGAGAGAAGCTCAAAATGTTACCAACAT 1039

Qy        321 GCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGAC 380

Db       1040 ACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTGCATCCCTTTTAC 1099

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Qy        441 CTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGA 500

Db       1160 CTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTATTGA 1219
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Qy        501 GAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCT 560
              |  |||||||  ||  | |||||    ||||||| |||||  |  | || |||||
Db       1220 ACGATATCAGCTGATTGTGAACCCCCGTGGCTGGAAACCCAGAGTAGCTCATGCCTATTG 1279

Qy        561 GGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAG 620
              ||||||  |  | || ||| |||||  |        | ||  | |||||  |      |
Db       1280 GGGGATCATCTTGATTTGGCTCATTTCTCTGACATTGTCTATTCCCTTATTCCTGTCCTA 1339

Qy        621 CATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAA 680
              | |||     ||||     |    | || | |||      ||   ||  ||    | |  |
Db       1340 CCACCTCACCAATGAGCCCTTTCATAATCTCTCTCTCCCTACTGACATCTACACCCACCA 1399

Qy        681 GGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCT 740
              ||| |  |||   |||  |||||        |   |||    | |||   | || |   |
Db       1400 GGTAGCTTGTGTGGAGATTTGGCCTTCTAAACTGAACCAACTCCTCTTTTCTACATCATT 1459

Qy        741 GCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTA 800
              |  |  |||||| |   |||| ||||| ||||| ||  ||||  ||        |||
Db       1460 ATTTATGCTCCAGTATTTTGTCCCTCTGGGTTTCATTCTTATCTGCTACCTGAAGATCGT 1519

Qy        801 CCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTG---CGAGC 857
              |   |||| |  |     |  | | ||| | | |   | |    |   ||
Db       1520 TCTCTGCCTCCGAAAAAGAACTAGGCAGGTGGACAGGAGAAAGGAAAATAAGAGCCGTCT 1579

Qy        858 TGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCT 917
                | |  |||  ||| |||||| || || |    || || ||| | ||||  |
Db       1580 CAATGAGAACAAGAGGGTAAATGTGATGTTGATTTCCATCGTAGTGACTTTTGGAGCCTG 1639

Qy        918 CTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCAT 977
              |||| ||||  || |  | |||||   | |     |||||| | ||||||    |    |
Db       1640 CTGGTTGCCCTTGAACATTTTCAATGTCATCTTCGACTGGTATCATGAGATGCTGATGAG 1699

Qy        978 CTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGT 1037
              |||||||     ||||  | ||  |||| |||||||| |||| ||||  || || ||| |
Db       1700 CTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGATTGCTATGGTTTCTACTTGCAT 1759

Qy       1038 CAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGT 1097
               || ||  || | ||||| ||||||||||  |||||| |||||| | | |   ||  |
Db       1760 AAATCCTCTCTTTTATGGATTTCTCAACAAAAACTTCCAGAAGGATCTAATGATGCTTAT 1819

Qy       1098 GCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGT 1157
              |    ||   |   | | || | |||    |  ||  || |  ||  |||| ||  |
Db       1820 TCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTATGAAAATATTGCCATGTCTACTAT 1879

Qy       1158 ACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTA 1214
              || || || |  ||||| || ||  | |  ||    ||   | |    ||| ||
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RESULT 9
US-08-894-236-5
; Sequence 5, Application US/08894236
; Patent No. 5939263
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/894,236
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,818
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  822..1937
US-08-894-236-5

  Query Match             21.1%;  Score 278.6;  DB 2;  Length 2280;
  Best Local Similarity   53.2%;  Pred. No. 1.4e-60;
  Matches  637;  Conservative    0;  Mismatches  554;  Indels    6;  Gaps    2;

Qy         24 GTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTTCACATC 83
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Db        740 GTTGTCCCTCAAGAACCAATGGCCAAACATCCACTGAGGATACACGGAAGCTTAGAAAAT 799

Qy         84 CACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAA 143
              | |||   | |   || || |  |||   ||||         |  |  |||    | |||
Db        800 CTCTAATTAAAATCCTGACATAATGGAAGTGCTCACAAACCAGCCAACACCTAATAAAAC 859

Qy        144 CAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGA 203
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Db        860 CAGTGGCAAGAGCAACAACTCGGCATTTTTCTACTTTGAATCCTGCCAACCCCCTTTTCT 919

Qy        204 CGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAA 263
              |  ||  |||| |  |||  | || |  |          || ||||  |  | || ||
Db        920 AGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTAATCATGGGCATTTTTGGAAA 979

Qy        264 CCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCC---AACGTGACCAACCT 320
              |||||  || ||      | |   | | | |  ||   ||||    || || |||||| |
Db        980 CCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAAGCTCAAAATGTTACCAACAT 1039

Qy        321 GCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGAC 380
              || || |||||||||  || |||||||| || |  ||||  || | |||   || | ||
Db       1040 ACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTGCATCCCTTTTAC 1099

Qy        381 CGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGC 440
              | | |||||||  | |||||| ||||| | |||||  | ||  | ||| ||  |  | |
Db       1100 GGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAACACTATGTGTAAACTCACTTC 1159

Qy        441 CTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGA 500
              || | | ||  |  | || ||  | || |||||  |||| || ||  |  | ||  | ||
Db       1160 CTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTATTGA 1219

Qy        501 GAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCT 560
              |  |||||||  ||  | |||||    |||||||| |||||  |  | || ||||
Db       1220 ACGATATCAGCTGATTGTGAACCCCCGTGGCTGGAAACCCAGAGTAGCTCATGCCTATTG 1279
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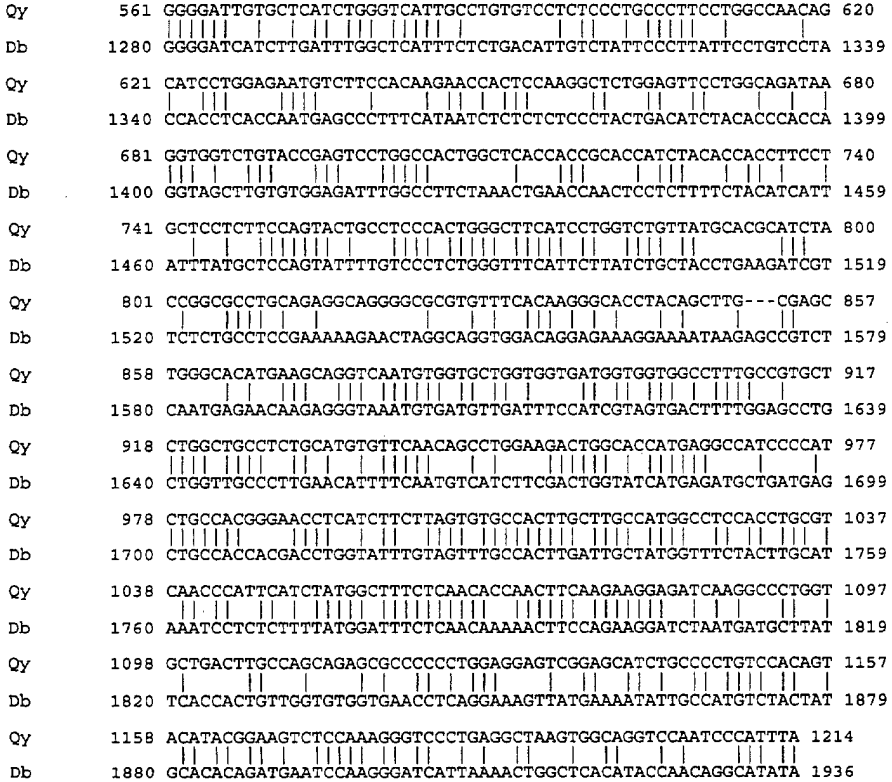

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RESULT 10
PCT-US96-01444-5
; Sequence 5, Application PC/TUS9601444
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01444
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,818
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  822..1937
PCT-US96-01444-5

  Query Match             21.1%;  Score 278.6;  DB 5;  Length 2280;
  Best Local Similarity   53.2%;  Pred. No. 1.4e-60;
  Matches  637;  Conservative    0;  Mismatches  554;  Indels    6;  Gaps    2;
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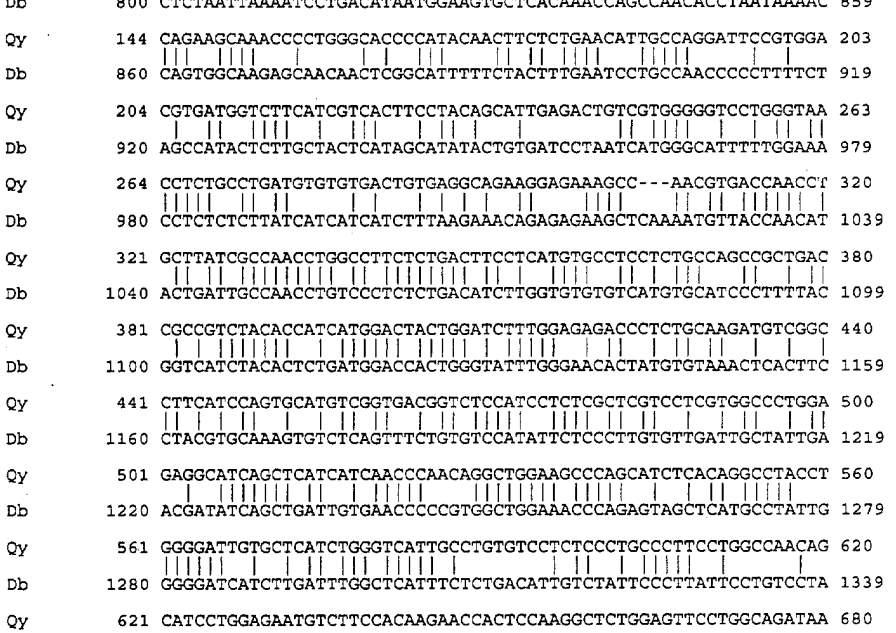
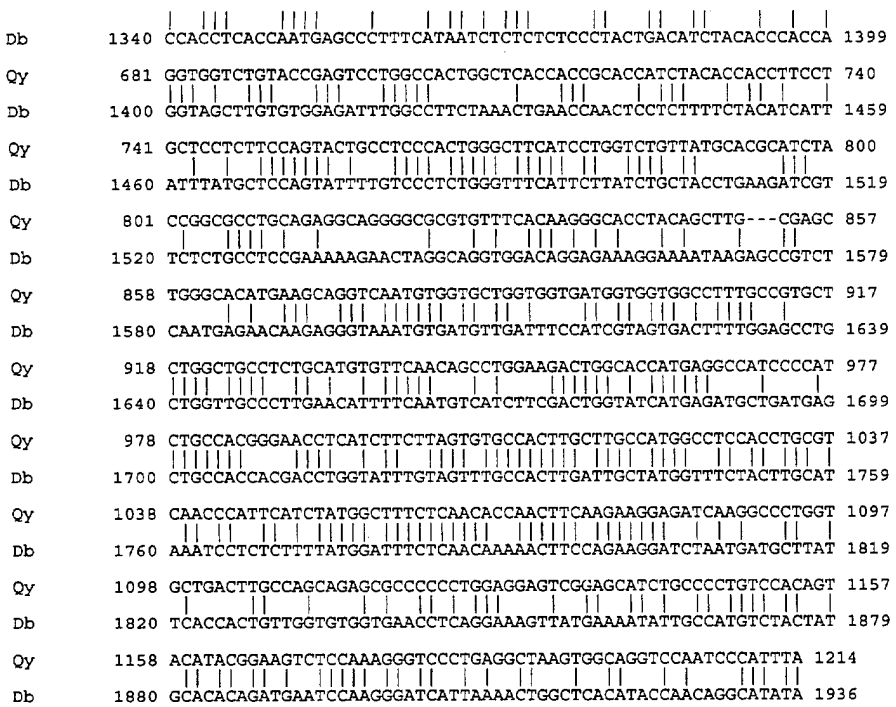
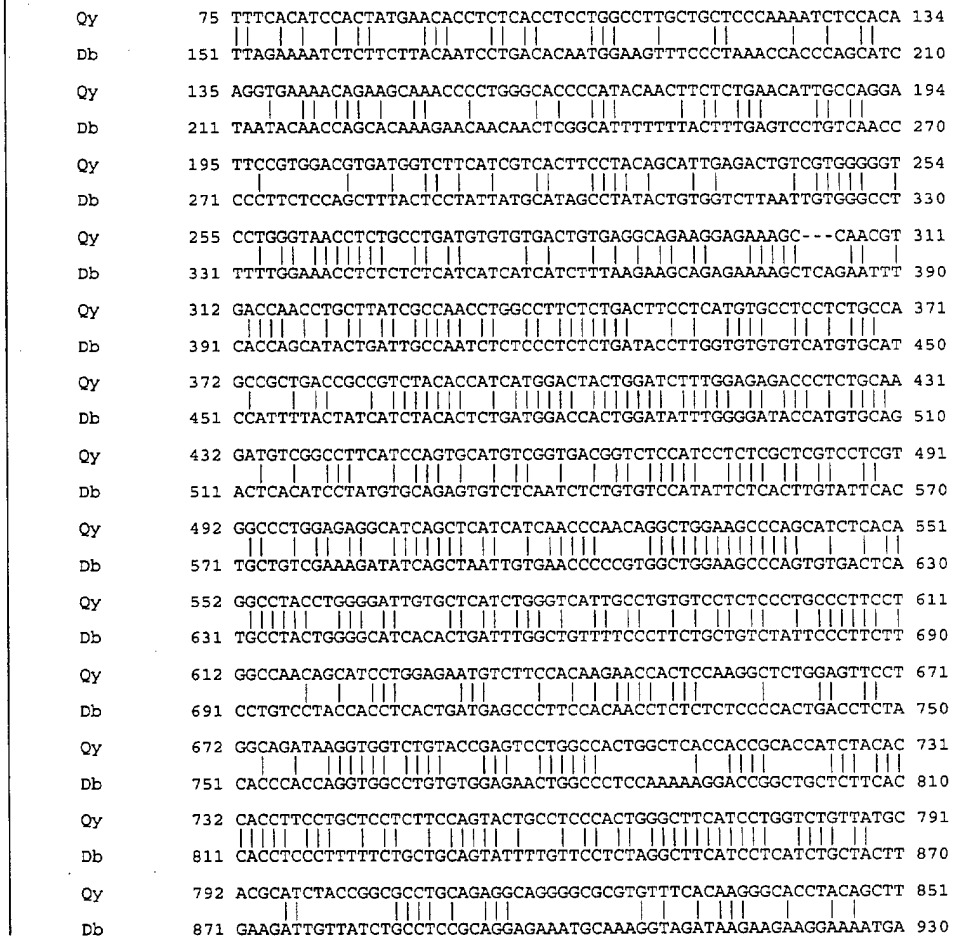




RESULT 11
US-08-415-818-11
; Sequence 11, Application US/08415818
; Patent No. 5621079
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,818
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1499 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-415-818-11

Query Match 20.2%; Score 266; DB 1; Length 1499;
Best Local Similarity 53.9%; Pred. No. 1.8e-57;
Matches 592; Conservative 0; Mismatches 500; Indels 6; Gaps 2;



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Db        931 GGGCCGGCTCAATGAGAACAAGAGGATCAACACAATGTTGATTTCCATCGTGGTGACCTT 990

Qy        909 TGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGC 968
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Db        991 TGGAGCCTGCTGGCTGCCCCCGAATATCTTCAATGTCATCTTTGACTGGTATCATGAGGT 1050

Qy        969 CATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTC 1028
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Db       1051 GCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGGTTGCTATGGTTTC 1110

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Db       1111 CACATGTATAAACCCTCTCTTTTATGGCTTTCTCAACAAAAATTTCCAAAAGGACCTGGT 1170

Qy       1089 GGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCT 1148
                | ||  | |     ||| |     | | || | |||    | ||  || |  || |
Db       1171 AGTGCTTATTCACCACTGCTGGTGCTTCACACCTCAGGAAAGATGTGAAAATATTGCCAT 1230

Qy       1149 GTCCACAGTACATACGGA 1166
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Db       1231 CTCCACTATGCACACAGA 1248


RESULT 12
US-08-894-236-11
; Sequence 11, Application US/08894236
; Patent No. 5939263
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/894,236
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,818
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1499 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-894-236-11

  Query Match             20.2%;  Score 266;  DB 2;  Length 1499;
  Best Local Similarity   53.9%;  Pred. No. 1.8e-57;
  Matches  592;  Conservative    0;  Mismatches  500;  Indels    6;  Gaps    2;

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Qy        135 AGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGA 194
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Db        211 TAATACAACCAGCACAAAGAACAACAACTCGGCATTTTTTTACTTTGAGTCCTGTCAACC 270

Qy        195 TTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGT 254
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Db        271 CCCTTCTCCAGCTTTACTCCTATTATGCATAGCCTATACTGTGGTCTTAATTGTGGGCCT 330

Qy        255 CCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGC---CAACGT 311
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Db        331 TTTTGGAAACCTCTCTCTCATCATCATCATCTTTAAGAAGCAGAGAAAAGCTCAGAATTT 390

Qy        312 GACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCA 371
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Db        451 CCATTTTACTATCATCTACACTCTGATGGACCACTGGATATTTGGGGATACCATGTGCAG 510

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Db        511 ACTCACATCCTATGTGCAGAGTGTCTCAATCTCTGTGTCCATATTCTCACTTGTATTCAC 570

Qy        492 GGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACA 551
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Qy        552 GGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCT 611
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Db        631 TGCCTACTGGGGCATCACACTGATTTGGCTGTTTTCCCTTCTGCTGTCTATTCCCTTCTT 690

Qy        612 GGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCT 671
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Db        691 CCTGTCCTACCACCTCACTGATGAGCCCTTCCACAACCTCTCTCTCCCCACTGACCTCTA 750

Qy        672 GGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACAC 731
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Db        751 CACCCACCAGGTGGCCTGTGTGGAGAACTGGCCCTCCAAAAAGGACCGGCTGCTCTTCAC 810

Qy        732 CACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGC 791
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Db        811 CACCTCCCTTTTTCTGCTGCAGTATTTTGTTCCTCTAGGCTTCATCCTCATCTGCTACTT 870

Qy        792 ACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTT 851
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Db        871 GAAGATTGTTATCTGCCTCCGCAGGAGAAATGCAAAGGTAGATAAGAAGAAGGAAAATGA 930

Qy        852 G---CGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTT 908
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Db        931 GGGCCGGCTCAATGAGAACAAGAGGATCAACACAATGTTGATTTCCATCGTGGTGACCTT 990

Qy        909 TGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGC 968
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Db       1051 GCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGGTTGCTATGGTTTC 1110

Qy       1029 CACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAA 1088
              ||| ||  | |||||  || | ||||||||||||||||  || ||| | |||||  |
Db       1111 CACATGTATAAACCCTCTCTTTTATGGCTTTCTCAACAAAAATTTCCAAAAGGACCTGGT 1170

Qy       1089 GGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCT 1148
              |  ||  | |    |||  |    | | || | |||    |  ||  ||  |  || |
Db       1171 AGTGCTTATTCACCACTGCTGGTGCTTCACACCTCAGGAAAGATGTGAAAATATTGCCAT 1230

Qy       1149 GTCCACAGTACATACGGA 1166
              |||||  | || || ||
Db       1231 CTCCACTATGCACACAGA 1248


RESULT 13
PCT-US96-01444-11
; Sequence 11, Application PC/TUS9601444
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01444
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,818
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1499 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US96-01444-11

  Query Match             20.2%;  Score 266;  DB 5;  Length 1499;
  Best Local Similarity   53.9%;  Pred. No. 1.8e-57;
  Matches  592;  Conservative    0;  Mismatches  500;  Indels    6;  Gaps    2;

Qy         75 TTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACA 134
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Db       151 TTAGAAAATCTCTTCTTACAATCCTGACACAATGGAAGTTTCCCTAAACCACCCAGCATC 210

Qy       135 AGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGA 194
               |  || ||| |  ||  |  | |  |||   | ||| |||    || ||
Db       211 TAATACAACCAGCACAAAGAACAACAACTCGGCATTTTTTTACTTTGAGTCCTGTCAACC 270

Qy       195 TTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGT 254
             |     |   |  || |  |  ||  |||| |  | |     | |||||  |
Db       271 CCCTTCTCCAGCTTTACTCCTATTATGCATAGCCTATACTGTGGTCTTAATTGTGGGCCT 330

Qy       255 CCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGC---CAACGT 311
             | || |||||||  || ||     | |  | | | || ||   |||||    ||  |
Db       331 TTTTGGAAACCTCTCTCTCATCATCATCATCTTTAAGAAGCAGAGAAAAGCTCAGAATTT 390

Qy       312 GACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCA 371
             ||||  | | || || ||||| ||  || |||||||    | |  ||||  || | |||
Db       391 CACCAGCATACTGATTGCCAATCTCTCCCTCTCTGATACCTTGGTGTGTGTCATGTGCAT 450

Qy       372 GCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAA 431
             |   |  ||   | |||||||  | ||||| |||||||  |||||  ||  |||  | ||||
Db       451 CCATTTTACTATCATCTACACTCTGATGGACCACTGGATATTTGGGGATACCATGTGCAG 510

Qy       432 GATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGT 491
             |  |  |||  | ||| |  | ||  |  | || |||||  |||| || ||  ||
Db       511 ACTCACATCCTATGTGCAGAGTGTCTCAATCTCTGTGTCCATATTCTCACTTGTATTCAC 570

Qy       492 GGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACA 551
             ||  | || ||  |||||||  ||  | |||||      |||||||||||||||  |  | ||
Db       571 TGCTGTCGAAAGATATCAGCTAATTGTGAACCCCCGTGGCTGGAAGCCCAGTGTGACTCA 630

Qy       552 GGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCT 611
             ||||||  ||| ||    || || ||| |  || ||  | | || ||  | | || |||||| |
Db       631 TGCCTACTGGGGCATCACACTGATTTGGCTGTTTTCCCTTCTGCTGTCTATTCCCTTCTT 690

Qy       612 GGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCT 671
                 |  | |||      |||    |  | |||| |||       |    ||  ||
Db       691 CCTGTCCTACCACCTCACTGATGAGCCCTTCCACAACCTCTCTCTCCCCACTGACCTCTA 750

Qy       672 GGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACAC 731
             |  |  |||||| |||   |||  ||||||      |  ||||    ||| |||
Db       751 CACCCACCAGGTGGCCTGTGTGGAGAACTGGCCCTCCAAAAAGGACCGGCTGCTCTTCAC 810

Qy       732 CACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGC 791
             ||||| |||  | ||  | |||||  |  | || || ||||||||||  ||||  ||
Db       811 CACCTCCCTTTTTCTGCTGCAGTATTTTGTTCCTCTAGGCTTCATCCTCATCTGCTACTT 870

Qy       792 ACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTT 851
                ||       ||||  |  |||       |  |  | |||   |   |  |
Db       871 GAAGATTGTTATCTGCCTCCGCAGGAGAAATGCAAAGGTAGATAAGAAGAAGGAAAATGA 930

Qy       852 G---CGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTT 908
             |   ||         | |  ||| | ||||    || ||  |   || |||||  ||||
Db       931 GGGCCGGCTCAATGAGAACAAGAGGATCAACACAATGTTGATTTCCATCGTGGTGACCTT 990

Qy       909 TGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGC 968
             ||  |    |||||||| | | || | ||||  | |    ||||| | |||||||
Db       991 TGGAGCCTGCTGGCTGCCCCCGAATATCTTCAATGTCATCTTTGACTGGTATCATGAGGT 1050

Qy       969 CATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTC 1028
             |  | ||||||      |||| | ||  |||| |||||||| |||| ||||  ||
Db      1051 GCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGGTTGCTATGGTTTC 1110

Qy      1029 CACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAA 1088
             ||| ||  | |||||  || | ||||||||||||||||  || ||| | |||||  |
Db      1111 CACATGTATAAACCCTCTCTTTTATGGCTTTCTCAACAAAAATTTCCAAAAGGACCTGGT 1170

Qy      1089 GGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCT 1148
             |  ||  | |    |||  |    | | || | |||    |  ||  ||  |  || |
Db      1171 AGTGCTTATTCACCACTGCTGGTGCTTCACACCTCAGGAAAGATGTGAAAATATTGCCAT 1230

Qy      1149 GTCCACAGTACATACGGA 1166
             |||||  | || || ||
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Db       1231 CTCCACTATGCACACAGA 1248

RESULT 14
US-09-045-186-1
; Sequence 1, Application US/09045186
; Patent No. 6087154
;  GENERAL INFORMATION:
;    APPLICANT:  Baez, Melvyn
;    APPLICANT:  Cates, Carolyn A.
;    TITLE OF INVENTION:  RHESUS NEUROPEPTIDE Y1 RECEPTOR
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lill Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/045,186
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaylo, Paul J.
;      REGISTRATION NUMBER:  36,808
;      REFERENCE/DOCKET NUMBER:  P-11376
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 276-0756
;      TELEFAX:  (317) 276-3861
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1152 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1152
US-09-045-186-1

  Query Match            19.5%;  Score 257.6;  DB 3;  Length 1152;
  Best Local Similarity  55.0%;  Pred. No. 2e-55;
  Matches  576;  Conservative    0;  Mismatches  459;  Indels   13;  Gaps    3;

Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239
Db         90 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 149

Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
Db        150 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCCTGAAACAAAAGGA 209

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
Db        210 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTCGC 269

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
Db        270 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 329

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
Db        330 GGCAATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 389

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db        390 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCTCGAGGGTGGAGACC 449

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db        450 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 509

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
Db        510 TCTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCGTTCCAAAATGTAAC 563

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719
Db        564 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 623

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
Db        624 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTTGGTCCACTTTGTTTTATATT 683

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836
Db        684 TATTTGCTACTTCAAGATATATATACGCTTAAAAAGGAGAAACAACATGATGGACAAGAT 743

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896
Db        744 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 803

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
Db        804 TGTGGTAGCATTTGCAGTCTGCTGGCTACCTCTTACCATCTTTAACACTGTGTTTGATTG 863

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
Db        864 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 923

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
Db        924 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGATTCCTGAACAAAAACTTCCA 983

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
Db        984 GAGAGACTTGCAGTTCTTCTTTAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1043

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db       1044 AACAATAGCCATGTCCACCATGCACACGGATGTTTCCAAGACTTCTTTGAAGCAA----G 1099

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224
Db       1100 CAAGCCCAGTCGCATTTAAAAAAATCAA 1127

RESULT 15
US-09-045-186-3
; Sequence 3, Application US/09045186
; Patent No. 6087154
;  GENERAL INFORMATION:
;    APPLICANT:  Baez, Melvyn
;    APPLICANT:  Cates, Carolyn A.
;    TITLE OF INVENTION:  RHESUS NEUROPEPTIDE Y1 RECEPTOR
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eli Lilly and Company
;      STREET:  Lill Corporate Center
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  United States of America
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/045,186
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: P-11376
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
US-09-045-186-3

Query Match 19.5%; Score 257.6; DB 3; Length 1152;
Best Local Similarity 38.0%; Pred. No. 2e-55;
Matches 398; Conservative 178; Mismatches 459; Indels 13; Gaps 3;

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Qy   240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
Db   150 GAUCAUUCUUGGUGUCUCUGGAAACCUGGCCUUGAUCAUAAUCAUCCUGAAACAAAAGGA 209

Qy   300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
Db   210 GAUGAGAAAUGUUACCAACAUCCUGAUUGUGAACCUUUCCUUCUCAGACUUGCUUGUCGC 269

Qy   360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
Db   270 CAUCAUGUGUCUCCCCUUUACAUUUGUCUACACAUUAAUGGACCACUGGGUCUUUGGUGA 329

Qy   420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
Db   330 GGCAAUGUGUAAGUUGAAUCCUUUUGUGCAAUGUGUUUCAAUCACUGUGUCCAUUUUCUC 389

Qy   480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db   390 UCUGGUUCUCAUUGCUGUGGAACGACAUCAGCUGAUAAUCAACCCUCGAGGGUGGAGACC 449

Qy   540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db   450 AAAUAAUAGACAUGCUUAUGUAGGUAUUGCUGUGAUUUGGGUCCUUGCUGUGGCUUCUUC 509

Qy   600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
Db   510 UCUGCCUUUCCUGAUCUACCAAGUAAUGACUGAUG------AGCCGUUCCAAAAUGUAAC 563

Qy   660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719
Db   564 ACUUGAUGCGUACAAAGACAAAUACGUGUGCUUUGAUCAAUUUCCAUCGGACUCUCAUAG 623

Qy   720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
Db   624 GUUGUCUUAUACCACUCUCCUCUUGGUGCUGCAGUAUUUUGGUCCACUUUGUUUUAUAUU 683

Qy   780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836
Db   684 UAUUUGCUACUUCAAGAUAUAUAUACGCUUAAAAAGGAGAAACAACAUGAUGGACAAGAU 743

Qy   837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896
Db   744 GAGAGACAAUAAGUACAGGUCCAGUGAAACCAAAAGAAUCAAUAUCAUGCUGCUCUCCAU 803

Qy   897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
Db   804 UGUGGUAGCAUUUGCAGUCUGCUGGCUACCUCUUACCAUCUUUAACACUGUGUUUGAUUG 863

Qy   957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
Db   864 GAAUCAUCAGAUCAUUGCUACCUGCAACCACAAUCUGUUAUUCCUGCUCUGCCACCUCAC 923

Qy  1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
Db   924 AGCAAUGAUAUCCACUUGUGUCAACCCCAUAUUUUAUGGAUUCCUGAACAAAAACUUCCA 983

Qy  1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
Db   984 GAGAGACUUGCAGUUCUUCUUUAACUUUUGUGAUUUCCGGUCUCGGGAUGAUGAUUAUGA 1043

Qy  1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db  1044 AACAAUAGCCAUGUCCACCAUGCACACGGAUGUUUCCAAGACUUCUUUGAAGCAA----G 1099

Qy  1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224
Db  1100 CAAGCCCAGUCGCAUUUAAAAAAAUCAA 1127
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Job time : 121 secs

OM nucleic - nucleic search, using sw model

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(without alignments)
10274.207 Million cell updates/sec

Title: US-09-430-775-1
Perfect score: 1320
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1210	91.7	1959	9	US-09-864-761-4424	Sequence 4424, Ap
	2	1180	89.4	1180	16	US-10-305-720-1061	Sequence 1061, Ap
	3	1128	85.5	1128	13	US-10-181-906-11	Sequence 11, Appl
	4	1128	85.5	1128	15	US-10-225-567A-202	Sequence 202, App
	5	959.4	72.7	983	9	US-09-864-761-21172	Sequence 21172, A
c	6	569.2	43.1	581	15	US-10-029-386-12634	Sequence 12634, A
	7	278.6	21.1	2281	9	US-09-900-497-1	Sequence 1, Appli
	8	257.6	19.5	1155	15	US-10-309-515-9	Sequence 9, Appli
	9	257.6	19.5	1155	15	US-10-126-764-9	Sequence 9, Appli
	10	257.6	19.5	1605	9	US-09-771-956-1	Sequence 1, Appli
	11	257.6	19.5	1605	12	US-10-410-648-3	Sequence 3, Appli
	12	257.6	19.5	1605	15	US-10-013-846-3	Sequence 3, Appli
	13	257.6	19.5	1605	15	US-10-083-245-1	Sequence 1, Appli
	14	257.6	19.5	1605	15	US-10-274-851-3	Sequence 3, Appli
	15	257.6	19.5	1605	15	US-10-291-446-1	Sequence 1, Appli
	16	257.6	19.5	1605	16	US-10-305-720-1231	Sequence 1231, Ap
	17	257.6	19.5	1888	15	US-10-176-847-25	Sequence 25, Appl
	18	257.6	19.5	2624	15	US-10-017-273A-2	Sequence 2, Appli
	19	257.6	19.5	2752	13	US-10-342-887-538	Sequence 538, App
	20	257.6	19.5	2752	13	US-10-172-118-538	Sequence 538, App
	21	257.6	19.5	2752	15	US-10-225-567A-377	Sequence 377, App
	22	257.6	19.5	2752	15	US-10-177-293-329	Sequence 329, App
	23	257.6	19.5	2752	16	US-10-295-027-639	Sequence 639, App
	24	257.6	19.5	2752	16	US-10-295-027-745	Sequence 745, App
	25	257.6	19.5	3210	15	US-10-198-846-11438	Sequence 11438, A
	26	255.6	19.4	1957	15	US-10-225-567A-375	Sequence 375, App
	27	255.6	19.4	1957	16	US-10-305-720-1169	Sequence 1169, Ap
	28	254	19.2	1952	13	US-10-181-906-15	Sequence 15, Appl
	29	253.8	19.2	1401	13	US-10-181-906-5	Sequence 5, Appli
	30	156	11.8	1110	14	US-10-044-592-17	Sequence 17, Appl
	31	156	11.8	1110	15	US-10-251-385-177	Sequence 177, App
	32	156	11.8	1110	15	US-10-278-087A-31	Sequence 31, Appl
	33	156	11.8	1113	15	US-10-225-567A-244	Sequence 244, App
	34	154.4	11.7	1331	14	US-10-044-592-73	Sequence 73, Appl
	35	152.8	11.6	1110	15	US-10-251-385-25	Sequence 25, Appl
	36	152.8	11.6	1535	16	US-10-305-720-1051	Sequence 1051, Ap
c	37	146	11.1	146	15	US-10-029-386-26334	Sequence 26334, A
	38	138.2	10.5	1293	9	US-09-866-248A-7	Sequence 7, Appli
	39	138.2	10.5	1293	15	US-10-225-567A-657	Sequence 657, App
	40	131.8	10.0	1320	9	US-09-292-973-3	Sequence 3, Appli
	41	128.2	9.7	1200	15	US-10-017-273A-3	Sequence 3, Appli
	42	128.2	9.7	1200	16	US-10-366-288-37	Sequence 37, Appl
	43	128.2	9.7	1200	16	US-10-305-720-1062	Sequence 1062, Ap
	44	128.2	9.7	1280	15	US-10-188-619-1	Sequence 1, Appli
	45	128.2	9.7	3241	13	US-10-181-906-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-864-761-4424
; Sequence 4424, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4424
;   LENGTH: 1959
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC006184.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;   NAME/KEY: unsure
;   LOCATION: 445
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;   LOCATION: 1856
US-09-864-761-4424

  Query Match            91.7%;  Score 1210;  DB 9;  Length 1959;
  Best Local Similarity  96.9%;  Pred. No. 0;
  Matches 1279;  Conservative    0;  Mismatches   34;  Indels    7;  Gaps    5;

Qy          1 AGTATTGTTTGTCTGTTTGCCTTGTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAA 60
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Qy        121 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 180
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Db        207 CCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCT 266

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Qy        241 ACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAG 300
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Db        387 AAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTNN 446

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Qy        841 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 900
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Db        927 ACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTG 986

Qy        901 GTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 960
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Db        987 GTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCAC 1046

Qy        961 CATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1020
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Db       1047 CATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCC 1106

Qy       1021 ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG 1080
              |||||||||||||| |||||||||||||||||||||||||||| ||||||||||||| ||
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Db       1283 TCCAATCCCATTTAACCAGGTCTAGGTCTTCTCCCTGCCATGTCCCTTGCCAGGGTTTTC 1342

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RESULT 2
US-10-305-720-1061
; Sequence 1061, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
;  TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
;  FILE REFERENCE: PA-0002-1 CON
;  CURRENT APPLICATION NUMBER: US/10/305,720
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: 09/016,434
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 1490
;  SOFTWARE: PERL Program
; SEQ ID NO 1061
;   LENGTH: 1180
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20040010136A1 g1063629
US-10-305-720-1061

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RESULT 3
US-10-181-906-11
; Sequence 11, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
;  APPLICANT: Karsenty, Gerard
;  APPLICANT:  Amling , Michael
;  APPLICANT:  Ducy, Patricia
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
;  TITLE OF INVENTION:  MODULATION OF NEUROPEPTIDE Y ACTIVITY
;  FILE REFERENCE: 9142-020-999
;  CURRENT APPLICATION NUMBER: US/10/181,906
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/US01/02040
;  PRIOR FILING DATE: 2001-01-22
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 1128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-181-906-11

  Query Match             85.5%;  Score 1128;  DB 13;  Length 1128;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy        268 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 327
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Qy        388 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 447
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Qy        628 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 687
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Db        541 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 600

Qy        688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 660

Qy        748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
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Db        661 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 720

Qy        808 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 780

Qy        868 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 840

Qy        928 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 900

Qy        988 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 1047
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Db        901 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 960

Qy       1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1020

Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1080

Qy       1168 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1215
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Db       1081 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1128
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RESULT 4
US-10-225-567A-202
; Sequence 202, Application US/10225567A
; Publication No. US20030113798A1

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; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
;   LENGTH: 1128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-202

  Query Match             85.5%;  Score 1128;  DB 15;  Length 1128;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGA 60

Qy        148 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTG 120

Qy        208 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTC 180

Qy        268 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATC 240

Qy        328 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 387
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Db        241 GCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTC 300

Qy        388 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 447
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Db        301 TACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATC 360

Qy        448 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 507
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCAT 420

Qy        508 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATT 480

Qy        568 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 627
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Db        481 GTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTG 540

Qy        628 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTC 600

Qy        688 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCTGCTCCTC 660

Qy        748 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 807
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTACCGGCGC 720

Qy        808 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 867
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Db        721 CTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTGCGAGCTGGGCACATG 780

Qy        868 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCT 840

Qy        928 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 987
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Db        841 CTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCATCTGCCACGGG 900

Qy        988 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 1047
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Db        901 AACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGTCAACCCATTC 960

Qy       1048 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1107
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Db        961 ATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGTGCTGACTTGC 1020

Qy       1108 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1167
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Db       1021 CAGCAGAGCGCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGTACATACGGAA 1080

Qy       1168 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1215
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Db       1081 GTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTAA 1128


RESULT 5
US-09-864-761-21172
; Sequence 21172, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21172
;   LENGTH: 983
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC006184.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;   OTHER INFORMATION: EST_HUMAN HIT: AW378515.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P50391, EVALUE 0.00e+00
;   OTHER INFORMATION: NT HIT: Z66526.1, EVALUE 0.00e+00
;   NAME/KEY: unsure
;   LOCATION: 308
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;   LOCATION: 867
US-09-864-761-21172

  Query Match             72.7%;  Score 959.4;  DB 9;  Length 983;
  Best Local Similarity   98.0%;  Pred. No. 9.8e-269;
  Matches  963;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy         52 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 111
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Db          1 TTAGTTCAAGAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCC 60

Qy        112 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 171
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Db         61 TTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATAC 120

Qy        172 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 231
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Db        121 AACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 180

Qy        232 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 291
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Db        181 AGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGG 240

Qy        292 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 351
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Db        241 CAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTC 300

Qy        352 CTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATC 411
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Db        301 CTCATGTNNCTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGATC 360

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Db        361 TTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCC 420

Qy        472 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 531
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Db        421 ATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGC 480

Qy        532 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 591
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Db        481 TGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGT 540

Qy        592 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 651
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Db        541 GTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCAC 600

Qy        652 TCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCT 711
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |
Db        601 TCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGNT 660

Qy        712 CACCACCGCACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGC 771
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Db        661 CACCACCGCACCATNTACACCACCTTCCTGCTCCTNTTCCAGTACTGCCTCCCACTGGGN 720

Qy        772 TTCATCCTGGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTT 831
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Db        721 TTCATNTTGGTCTGTTATGCACGCATNTACCGGTGCCTGCAGAGGCAGGGGCGCGTGTTT 780

Qy        832 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 891
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Db        781 CACAAGGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTG 840

Qy        892 GTGATGGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 951
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        841 GTGATGGTGGTGGCCTTTGCCGTGCTNTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAA 900

Qy        952 GACTGGCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCAC 1011
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Db        901 GACTGGCACCATGAGGCCATCCCCATCTGCCATGGGAACCTCATCTTCTTAGTGTGCCAC 960

Qy       1012 TTGCTTGCCATGGCCTCCACCTG 1034
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Db        961 TTGCTTGCCATGGCCTCCACCTG 983
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RESULT 6
US-10-029-386-12634/c
; Sequence 12634, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12634
;   LENGTH: 581
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR10.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.49
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
;   OTHER INFORMATION: EST_HUMAN HIT: BG875680.1, EVALUE 0.00e+00
;   OTHER INFORMATION: NT HIT: Z66526.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P50391, EVALUE 5.00e-97
;   NAME/KEY: unsure
;   LOCATION: 319
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;   LOCATION: 332
;   NAME/KEY: unsure
;   LOCATION: 333
US-10-029-386-12634

  Query Match           43.1%;  Score 569.2;  DB 15;  Length 581;
  Best Local Similarity   98.3%;  Pred. No. 3.3e-155;
  Matches  571;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        111 CTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATA 170
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Db        581 CTTGCTGCTCCCAAAATCTCCACAAGGTGAAAACAGAAGCAAACCCCTGGGCACCCCATA 522

Qy        171 CAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTA 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 CAACTTCTCTGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTA 462

Qy        231 CAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAG 290
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Db        461 CAGCATTGAGACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAG 402

Qy        291 GCAGAAGGAGAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTT 350
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Qy        351 CCTCATGTGCCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGAT 410
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Db        341 CCTCATGTNNCTNNNTTGNCAGNCGGTGACCGCCGTCTACACCATCATGGACTACTGGAT 282

Qy        411 CTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CTTTGGAGAGACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTC 222

Qy        471 CATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGG 530
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Db        221 CATCCTCTCGCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGG 162

Qy        531 CTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTG 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 CTGGAAGCCCAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTG 102

Qy        591 TGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCA 650
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Db        101 TGTCCTCTCCCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCA 42

Qy        651 CTCCAAGGCTCTGGAGTTCCTGGCAGATAAGGTGGTCTGTA 691
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Db         41 CTCCAAGGCTCTGGAGTTCCTGGCGGATAAGGTGGTCTGTA 1
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RESULT 7
US-09-900-497-1
; Sequence 1, Application US/09900497
; Patent No. US20020082232A1
; GENERAL INFORMATION:
;  APPLICANT: Allen, Keith D.
;  TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NPY6-R
;  TITLE OF INVENTION:  NEUROPEPTIDE RECEPTOR GENE DISRUPTIONS
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;  FILE REFERENCE: R-639
;  CURRENT APPLICATION NUMBER: US/09/900,497
;  CURRENT FILING DATE:  2001-07-06
;  PRIOR APPLICATION NUMBER: US 60/216,260
;  PRIOR FILING DATE: 2000-07-06
;  PRIOR APPLICATION NUMBER: US 60/221,474
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2281
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-900-497-1

  Query Match             21.1%;  Score 278.6;  DB 9;  Length 2281;
  Best Local Similarity   53.2%;  Pred. No. 2.2e-70;
  Matches  637;  Conservative    0;  Mismatches  554;  Indels    6;  Gaps    2;

Qy         24 GTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAATCTTTTCACATC 83
              ||  |  | |||      |||  |    ||  |       ||  |  |  |  |  ||  | |
Db        741 GTTGTCCCTCAAGAACCAATGGCCAAACATCCACTGAGGATACACGGAAGCTTAGAAAAT 800

Qy         84 CACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTCCCAAAATCTCCACAAGGTGAAAA 143
              | |||    | |   || || |  |||   ||||      |   |  |||     | |||
Db        801 CTCTAATTAAAATCCTGACATAATGGAAGTGCTCACAAACCAGCCAACACCTAATAAAAC 860

Qy        144 CAGAAGCAAACCCCTGGGCACCCCATACAACTTCTCTGAACATTGCCAGGATTCCGTGGA 203
              |||  ||||    |    | |  |||    || ||  ||||   |||||      |  |
Db        861 CAGTGGCAAGAGCAACAACTCGGCATTTTTCTACTTTGAATCCTGCCAACCCCCTTTTCT 920

Qy        204 CGTGATGGTCTTCATCGTCACTTCCTACAGCATTGAGACTGTCGTGGGGGTCCTGGGTAA 263
              |  ||  ||||  |  |||   | || |   |      || ||||  |  | || ||
Db        921 AGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTAATCATGGGCATTTTTGGAAA 980

Qy        264 CCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGAGAAAGCC---AACGTGACCAACCT 320
              |||||  || ||      | |   | | | |  ||     ||||    || || |||||| |
Db        981 CCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAAGCTCAAAATGTTACCAACAT 1040

Qy        321 GCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTGCCTCCTCTGCCAGCCGCTGAC 380
              || || |||||||||  || ||||||||  || |  ||||  || | |||   ||  | ||
Db       1041 ACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTGCATCCCTTTTAC 1100

Qy        381 CGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGAGACCCTCTGCAAGATGTCGGC 440
              | | |||||||  | |||||| |||||  | |||||  | ||  | ||  ||  |  | |
Db       1101 GGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAACACTATGTGTAAACTCACTTC 1160

Qy        441 CTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTCGCTCGTCCTCGTGGCCCTGGA 500
              || | | ||   |  | || ||  | || ||||  |||| || ||   |  | ||  | ||
Db       1161 CTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTATTGA 1220

Qy        501 GAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCCCAGCATCTCACAGGCCTACCT 560
                |  ||||||| ||   | |||||     |||||||| |||||  |  | || |||||
Db       1221 ACGATATCAGCTGATTGTGAACCCCCGTGGCTGGAAACCCAGAGTAGCTCATGCCTATTG 1280

Qy        561 GGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTCCCTGCCCTTCCTGGCCAACAG 620
              ||||||  |  | || ||| ||||| |          |||  | |||||  |    |  |
Db       1281 GGGGATCATCTTGATTTGGCTCATTTCTCTGACATTGTCTATTCCCTTATTCCTGTCCTA 1340

Qy        621 CATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGCTCTGGAGTTCCTGGCAGATAA 680
              |  |||      ||||     |   | || | |||      ||   ||  ||     |  |  |
Db       1341 CCACCTCACCAATGAGCCCTTTCATAATCTCTCTCTCCCTACTGACATCTACACCCACCA 1400

Qy        681 GGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCGCACCATCTACACCACCTTCCT 740
              |||  |  |||   |||   |||||     |  |||   | |||  | || |   |
Db       1401 GGTAGCTTGTGTGGAGATTTGGCCTTCTAAACTGAACCAACTCCTCTTTTCTACATCATT 1460

Qy        741 GCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCTGGTCTGTTATGCACGCATCTA 800
              |   |  |||||||  |   |||| |||||  ||  ||||  ||         |||
Db       1461 ATTTATGCTCCAGTATTTTGTCCCTCTGGGTTTCATTCTTATCTGCTACCTGAAGATCGT 1520

Qy        801 CCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAAGGGCACCTACAGCTTG---CGAGC 857
                |  |||| |  |          |  | |  ||| | | |   | |    |   ||
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Db       1521 TCTCTGCCTCCGAAAAAGAACTAGGCAGGTGGACAGGAGAAAGGAAAATAAGAGCCGTCT 1580

Qy        858 TGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGATGGTGGTGGCCTTTGCCGTGCT 917
                | |  |||  ||| |||||| || ||  |     || ||  ||| | ||||  |
Db       1581 CAATGAGAACAAGAGGGTAAATGTGATGTTGATTTCCATCGTAGTGACTTTTGGAGCCTG 1640

Qy        918 CTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGCCATCCCCAT 977
              ||||  ||||  ||  |  | |||||   | |   ||||||  | ||||||    |  . |
Db       1641 CTGGTTGCCCTTGAACATTTTCAATGTCATCTTCGACTGGTATCATGAGATGCTGATGAG 1700

Qy        978 CTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCTTGCCATGGCCTCCACCTGCGT 1037
              |||||||    ||||  | ||  |||| |||||||| |||| ||||  || || ||| |
Db       1701 CTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTGATTGCTATGGTTTCTACTTGCAT 1760

Qy       1038 CAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAGGAGATCAAGGCCCTGGT 1097
              || ||  || | ||||| |||||||||| ||||||  |||||||  | | |   ||  |
Db       1761 AAATCCTCTCTTTTATGGATTTCTCAACAAAAACTTCCAGAAGGATCTAATGATGCTTAT 1820

Qy       1098 GCTGACTTGCCAGCAGAGCGCCCCCCCTGGAGGAGTCGGAGCATCTGCCCCTGTCCACAGT 1157
              |     ||    |    | | || | |||    |  || || |  || |||| || |
Db       1821 TCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTATGAAAATATTGCCATGTCTACTAT 1880

Qy       1158 ACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAATCCCATTTA 1214
              || || || |  ||||| || ||  | |  ||  |   ||  |  |||  ||
Db       1881 GCACACAGATGAATCCAAGGGATCATTAAAACTGGCTCACATACCAACAGGCATATA 1937


RESULT 8
US-10-309-515-9
; Sequence 9, Application US/10309515
; Publication No. US20030114644A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin M.
;  APPLICANT:  Waters, Stephen M.
;  APPLICANT:  Krause, James E.
;  TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
;  FILE REFERENCE: N00.2102C1
;  CURRENT APPLICATION NUMBER: US/10/309,515
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  PRIOR APPLICATION NUMBER: 10/126,764
;  PRIOR FILING DATE: 2002-04-18
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 1155
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-309-515-9

  Query Match             19.5%;  Score 257.6;  DB 15;  Length 1155;
  Best Local Similarity   55.0%;  Pred. No. 2.2e-64;
  Matches  576;  Conservative    0;  Mismatches  459;  Indels   13;  Gaps    3;

Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239
              |||  |||| ||     || ||| | ||||  |  | |  |  | ||  |  ||
Db         90 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 149

Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
              ||   |  | || |||   || |||||    | ||||      | |   |||  || |||||
Db        150 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 209

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
              ||      || || ||||| | || || |  |||||  ||||||  ||||| ||   |
Db        210 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 269

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
              | || | || |   ||  | ||     |||||||  | ||||||  |||||  |||||| ||
Db        270 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 329

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
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Db        330 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 389

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539

Db        390 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCTCGAGGGTGGAGACC 449

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599

Db        450 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 509

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659

Db        510 TTTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCGTTCCAAAATGTAAC 563

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719

Db        564 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 623

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779

Db        624 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTTGGTCCACTTTGTTTTATATT 683

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836

Db        684 TATTTGCTACTTCAAGATATATATACGCCTAAAAAGGAGAAACAACATGATGGACAAGAT 743

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896

Db        744 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 803

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956

Db        804 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 863

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016

Db        864 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 923

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076

Db        924 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 983

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136

Db        984 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1043

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196

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Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224

Db       1100 CAAGCCCAGTCGCATTTAAAAAAATCAA 1127


RESULT 9
US-10-126-764-9
; Sequence 9, Application US/10126764
; Publication No. US20030166834A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett Kinrade, Michele
;  APPLICANT:  Brodbeck, Robbin
;  APPLICANT:  Krause, James
;  TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
;  FILE REFERENCE: N00.2102
;  CURRENT APPLICATION NUMBER: US/10/126,764
;  CURRENT FILING DATE:  2002-04-18
;  PRIOR APPLICATION NUMBER: 60/284,835
;  PRIOR FILING DATE: 2001-04-19
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;  LENGTH: 1155
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-126-764-9

  Query Match            19.5%;  Score 257.6;  DB 15;  Length 1155;
  Best Local Similarity  55.0%;  Pred. No. 2.2e-64;
  Matches  576;  Conservative    0;  Mismatches  459;  Indels   13;  Gaps    3;

Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239

Db         90 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 149

Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299

Db        150 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 209

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359

Db        210 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 269

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419

Db        270 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 329

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479

Db        330 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 389

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539

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Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659

Db        510 TTTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCGTTCCAAAATGTAAC 563

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719

Db        564 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 623

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779

Db        624 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTTGGTCCACTTTGTTTTATATT 683

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836

Db        684 TATTTGCTACTTCAAGATATATATACGCCTAAAAAGGAGAAACAACATGATGGACAAGAT 743

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896

Db        744 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 803

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956

Db        804 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 863

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016

Db        864 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 923

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076

Db        924 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 983

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136

Db        984 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1043
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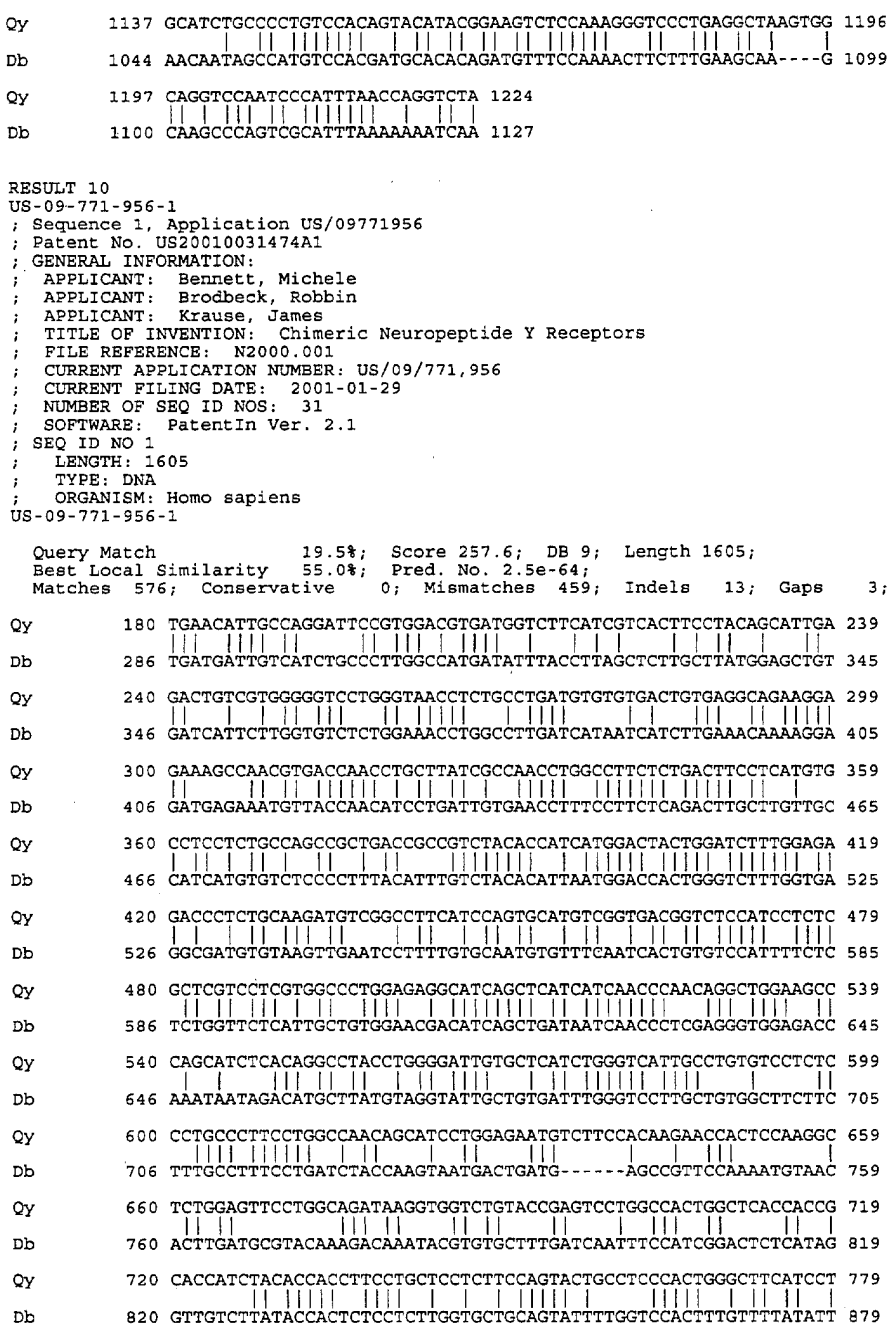
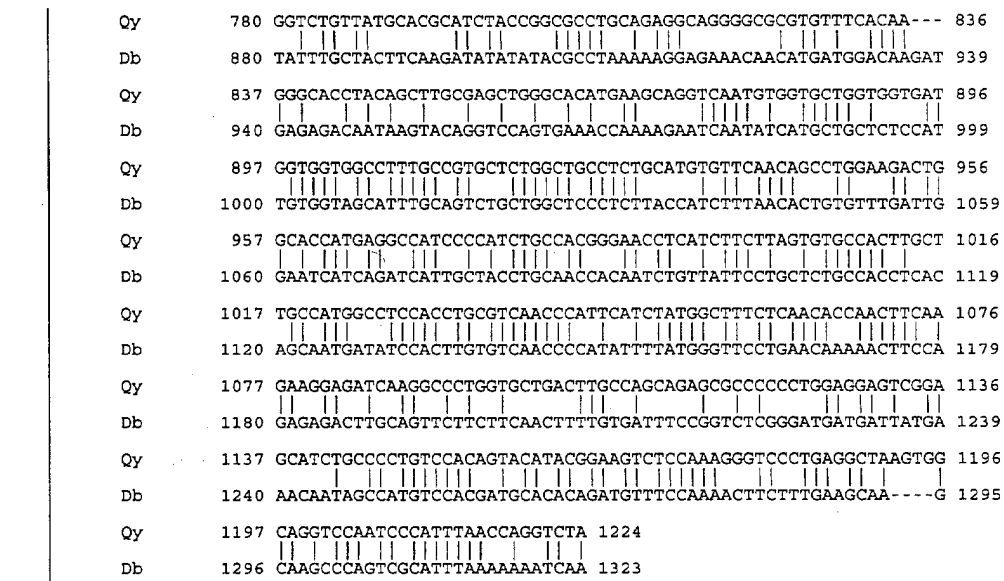


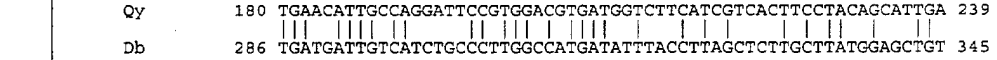
RESULT 10
US-09-771-956-1
; Sequence 1, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-956-1

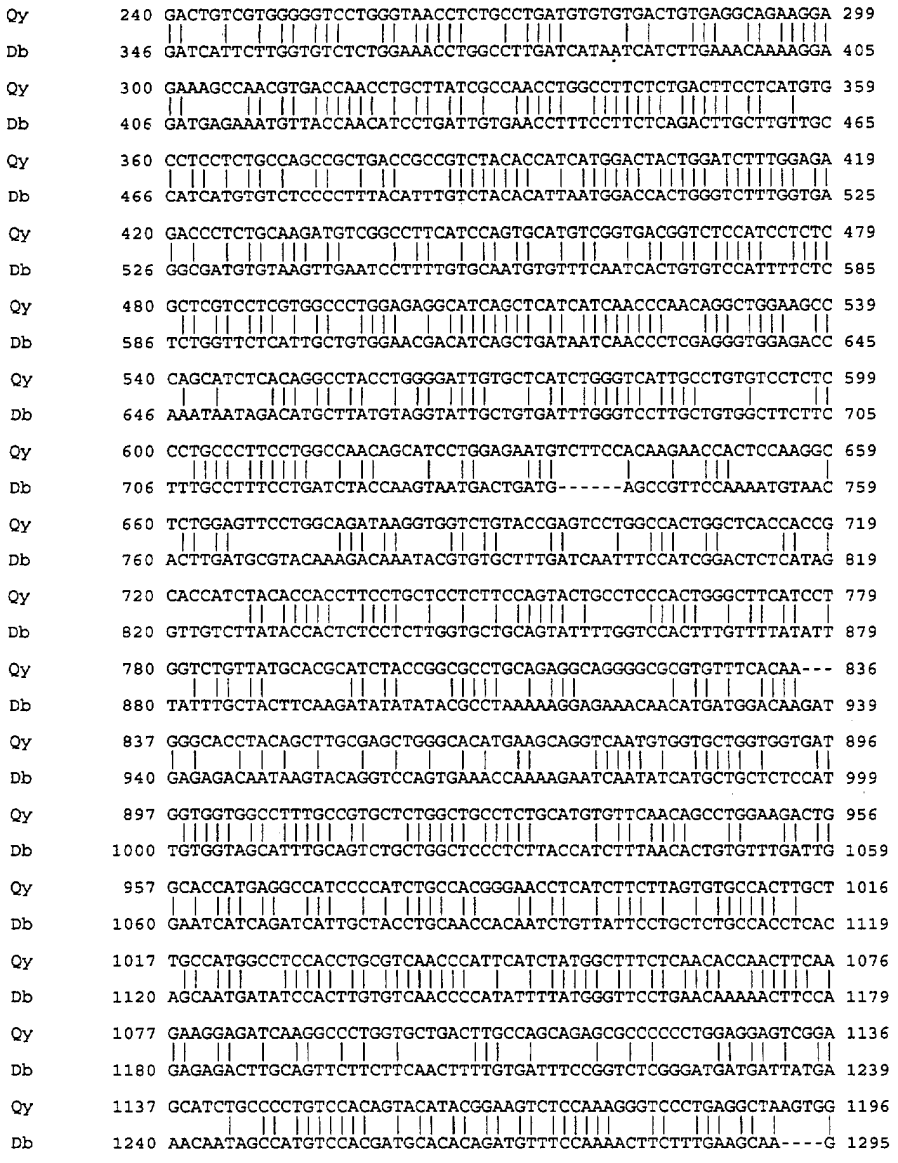
Query Match 19.5%; Score 257.6; DB 9; Length 1605;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;



RESULT 11
US-10-410-648-3
; Sequence 3, Application US/10410648
; Publication No. US20040072847A1
; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A.
; APPLICANT: Brielmann, Harry L.
; APPLICANT: Darrow, James W.
; APPLICANT: De Lombaert, Stephane W.
; APPLICANT: Hutchinson, Alan W.
; APPLICANT: Tran, Jennifer W.
; APPLICANT: Zheng, Xiaozhang W.
; APPLICANT: Elliott, Richard L.
; APPLICANT: Hammond, Marlys L.
; TITLE OF INVENTION: SPIRO[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
; TITLE OF INVENTION: 3H-SPIROISOBENZOFURAN-1,4'-PIPERIDINES
; FILE REFERENCE: U 014539-7
; CURRENT APPLICATION NUMBER: US/10/410,648
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/013,846
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-648-3

Query Match 19.5%; Score 257.6; DB 12; Length 1605;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;

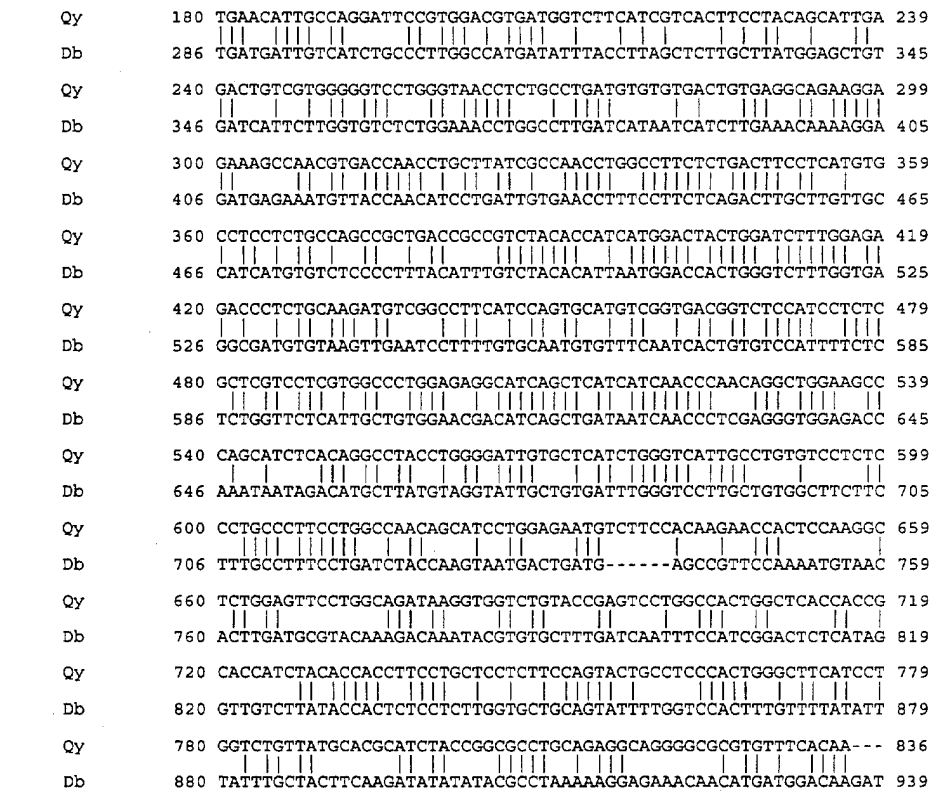




RESULT 12
US-10-013-846-3
; Sequence 3, Application US/10013846
; Publication No. US20030036652A1

; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Brielmann, Harry L
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Marlys
; TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
; TITLE OF INVENTION: 3H-spiroisobenzofuran-1,4'-piperidines
; FILE REFERENCE: N00.2001
; CURRENT APPLICATION NUMBER: US/10/013,846
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-846-3

Query Match 19.5%; Score 257.6; DB 15; Length 1605;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;



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Db        940 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 999

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
Db       1000 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 1059

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
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Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
Db       1120 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 1179

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
Db       1180 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1239

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db       1240 AACAATAGCCATGTCCACGATGCACACAGATGTTTCCAAAACTTCTTTGAAGCAA----G 1295

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224
Db       1296 CAAGCCCAGTCGCATTTAAAAAAATCAA 1323
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RESULT 13
US-10-083-245-1
; Sequence 1, Application US/10083245
; Publication No. US20030069246A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, James W.
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Blum, Charles
; APPLICANT: Tran, Jennifer
; APPLICANT: Giangiordano, Mark
; APPLICANT: Griffith, David Andrew
; APPLICANT: Carpino, Philip Albert
; TITLE OF INVENTION: Certain Alkylene Diamine-Substituted Pyrazolo
; TITLE OF INVENTION: [1,5,-a]-1,5-Pyrimidines and pyrazolo
; TITLE OF INVENTION: [1,5-a]-1,3,5-Triazines
; FILE REFERENCE: U012955-3
; CURRENT APPLICATION NUMBER: US/10/083,245
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US/09/676,970
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-083-245-1

Query Match 19.5%; Score 257.6; DB 15; Length 1605;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;

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Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239
Db        286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy        240 GACTGTCGTGGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
Db        346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
Db        406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
Db        466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
Db        526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db        586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCTCGAGGGTGGAGACC 645

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db        646 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 705

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
Db        706 TTTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCGTTCCAAAATGTAAC 759

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719
Db        760 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 819

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
Db        820 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTTGGTCCACTTTGTTTTATATT 879

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836
Db        880 TATTTGCTACTTCAAGATATATATACGCCTAAAAAGGAGAAACAACATGATGGACAAGAT 939

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896
Db        940 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 999

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
Db       1000 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 1059

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
Db       1060 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 1119

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
Db       1120 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 1179

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
Db       1180 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1239

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db       1240 AACAATAGCCATGTCCACGATGCACACAGATGTTTCCAAAACTTCTTTGAAGCAA----G 1295

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224
Db       1296 CAAGCCCAGTCGCATTTAAAAAAATCAA 1323
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RESULT 14
US-10-274-851-3
; Sequence 3, Application US/10274851
; Publication No. US20030144290A1
; GENERAL INFORMATION:
; APPLICANT: Blum, Charles
; APPLICANT: Brielmann, Harry
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Zheng, Xiaozhang
; TITLE OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE
; TITLE OF INVENTION: DERIVATIVES

```
;  FILE REFERENCE: U 014209-8
;  CURRENT APPLICATION NUMBER: US/10/274,851
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-274-851-3

  Query Match            19.5%;  Score 257.6;  DB 15;  Length 1605;
  Best Local Similarity  55.0%;  Pred. No. 2.5e-64;
  Matches  576;  Conservative    0;  Mismatches  459;  Indels   13;  Gaps    3;

Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239
Db        286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy        240 GACTGTCGTGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
Db        346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
Db        406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
Db        466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
Db        526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db        586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCTCGAGGGTGGAGACC 645

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db        646 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 705

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
Db        706 TTTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCGTTCCAAAATGTAAC 759

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719
Db        760 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 819

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779
Db        820 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTGGTCCACTTTGTTTTATATT 879

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836
Db        880 TATTTGCTACTTCAAGATATATATACGCCTAAAAAGGAGAAACAACATGATGGACAAGAT 939

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896
Db        940 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 999

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956
Db       1000 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 1059

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016
Db       1060 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 1119

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076
Db       1120 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 1179

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136
Db       1180 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1239

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db       1240 AACAATAGCCATGTCCACGATGCACACAGATGTTTCCAAAACTTCTTTGAAGCAA----G 1295

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224
Db       1296 CAAGCCCAGTCGCATTTAAAAAAATCAA 1323

RESULT 15
US-10-291-446-1
; Sequence 1, Application US/10291446
; Publication No. US20030158197A1
; GENERAL INFORMATION:
;  APPLICANT: Horvath, Raymond F.
;  APPLICANT:  Tran, Jennifer
;  APPLICANT:  De Lombaert, Stephane
;  APPLICANT:  Hodgetts, Kevin J.
;  APPLICANT:  Carpino, Philip A.
;  APPLICANT:  Griffith, David A.
;  TITLE OF INVENTION: Certain Alkylene Diamine-Substituted Heterocycles
;  FILE REFERENCE: U 014242-0
;  CURRENT APPLICATION NUMBER: US/10/291,446
;  CURRENT FILING DATE:  2002-11-08
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-10-291-446-1

  Query Match            19.5%;  Score 257.6;  DB 15;  Length 1605;
  Best Local Similarity  55.0%;  Pred. No. 2.5e-64;
  Matches  576;  Conservative    0;  Mismatches  459;  Indels   13;  Gaps    3;

Qy        180 TGAACATTGCCAGGATTCCGTGGACGTGATGGTCTTCATCGTCACTTCCTACAGCATTGA 239
Db        286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy        240 GACTGTCGTGGGGTCCTGGGTAACCTCTGCCTGATGTGTGTGACTGTGAGGCAGAAGGA 299
Db        346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy        300 GAAAGCCAACGTGACCAACCTGCTTATCGCCAACCTGGCCTTCTCTGACTTCCTCATGTG 359
Db        406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy        360 CCTCCTCTGCCAGCCGCTGACCGCCGTCTACACCATCATGGACTACTGGATCTTTGGAGA 419
Db        466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy        420 GACCCTCTGCAAGATGTCGGCCTTCATCCAGTGCATGTCGGTGACGGTCTCCATCCTCTC 479
Db        526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy        480 GCTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCATCAACCCAACAGGCTGGAAGCC 539
Db        586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCCTCGAGGGTGGAGACC 645

Qy        540 CAGCATCTCACAGGCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCTGTGTCCTCTC 599
Db        646 AAATAATAGACATGCTTATGTAGGTATTGCTGTGATTTGGGTCCTTGCTGTGGCTTCTTC 705

Qy        600 CCTGCCCTTCCTGGCCAACAGCATCCTGGAGAATGTCTTCCACAAGAACCACTCCAAGGC 659
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Db        706 TTTGCCTTTCCTGATCTACCAAGTAATGACTGATG------AGCCGTTCCAAAATGTAAC 759

Qy        660 TCTGGAGTTCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGCTCACCACCG 719

Db        760 ACTTGATGCGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG 819

Qy        720 CACCATCTACACCACCTTCCTGCTCCTCTTCCAGTACTGCCTCCCACTGGGCTTCATCCT 779

Db        820 GTTGTCTTATACCACTCTCCTCTTGGTGCTGCAGTATTTTGGTCCACTTTGTTTTATATT 879

Qy        780 GGTCTGTTATGCACGCATCTACCGGCGCCTGCAGAGGCAGGGGCGCGTGTTTCACAA--- 836

Db        880 TATTTGCTACTTCAAGATATATATACGCCTAAAAAGGAGAAACAACATGATGGACAAGAT 939

Qy        837 GGGCACCTACAGCTTGCGAGCTGGGCACATGAAGCAGGTCAATGTGGTGCTGGTGGTGAT 896

Db        940 GAGAGACAATAAGTACAGGTCCAGTGAAACCAAAAGAATCAATATCATGCTGCTCTCCAT 999

Qy        897 GGTGGTGGCCTTTGCCGTGCTCTGGCTGCCTCTGCATGTGTTCAACAGCCTGGAAGACTG 956

Db       1000 TGTGGTAGCATTTGCAGTCTGCTGGCTCCCTCTTACCATCTTTAACACTGTGTTTGATTG 1059

Qy        957 GCACCATGAGGCCATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGCT 1016

Db       1060 GAATCATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCCTGCTCTGCCACCTCAC 1119

Qy       1017 TGCCATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAA 1076

Db       1120 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTTCCTGAACAAAAACTTCCA 1179

Qy       1077 GAAGGAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCCTGGAGGAGTCGGA 1136

Db       1180 GAGAGACTTGCAGTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGGATGATGATTATGA 1239

Qy       1137 GCATCTGCCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196

Db       1240 AACAATAGCCATGTCCACGATGCACACAGATGTTTCCAAAACTTCTTTGAAGCAA----G 1295

Qy       1197 CAGGTCCAATCCCATTTAACCAGGTCTA 1224

Db       1296 CAAGCCCAGTCGCATTTAAAAAAATCAA 1323
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Search completed: May 11, 2004, 11:01:35
Job time : 588 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:36 ; Search time 58 Seconds
(without alignments)
1826.816 Million cell updates/sec

Title: US-09-430-775-2
Perfect score: 1965
Sequence: 1 MNTSHLLALLLPKSPQGENR.....TVHTEVSKGSLRLSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1965	100.0	375	4	AAE06691	Aae06691 Human neu
2	1965	100.0	375	5	ABB84501	Abb84501 Human hip
3	1965	100.0	375	6	ABP81859	Abp81859 Human neu
4	1956	99.5	375	2	AAR79119	Aar79119 Neuropept
5	1519	77.3	375	6	ABG73516	Abg73516 Murine NY
6	1494	76.0	375	2	AAR79120	Aar79120 Neuropept
7	1494	76.0	375	6	ABG73517	Abg73517 Rat NY4R
8	960	48.9	375	6	ABG73520	Abg73520 D. rerio
9	869	44.2	382	4	AAE08001	Aae08001 Rat neuro
10	867.5	44.1	383	6	ABG73519	Abg73519 C. porcel
11	867	44.1	382	2	AAW02101	Aaw02101 Mouse neu
12	863	43.9	371	2	AAW02099	Aaw02099 Mouse neu
13	860.5	43.8	384	5	ABB84499	Abb84499 Human hip
14	856.5	43.6	383	3	AAB14324	Aab14324 Rhesus Y1
15	856.5	43.6	384	2	AAR35493	Aar35493 Human NPY
16	856.5	43.6	384	2	AAR35494	Aar35494 Human NPY
17	856.5	43.6	384	4	AAE07956	Aae07956 Human neu
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20	856.5	43.6	384	4	AAB85108	Aab85108 Human neu
21	856.5	43.6	384	4	AAE08000	Aae08000 Human neu
22	856.5	43.6	384	5	AAU10585	Aau10585 Human neu
23	856.5	43.6	384	5	ABB79509	Abb79509 Human neu
24	856.5	43.6	384	6	ABJ37037	Abj37037 Human bre
25	856.5	43.6	384	6	ABR47546	Abr47546 Breast ca
26	856.5	43.6	384	6	ABP81946	Abp81946 Human neu
27	856.5	43.6	384	6	AAO23265	Aao23265 Human neu
28	856.5	43.6	384	7	ABW01461	Abw01461 Human neu
29	855	43.5	398	2	AAW03014	Aaw03014 Modified
30	854.5	43.5	411	2	AAW03012	Aaw03012 Neuropept
31	847	43.1	371	6	ABG73518	Abg73518 Rabbit NY
32	846.5	43.1	388	4	AAE06688	Aae06688 Human neu
33	841	42.8	383	2	AAR43913	Aar43913 Sequence
34	830.5	42.3	399	2	AAW03013	Aaw03013 Modified
35	823.5	41.9	370	2	AAW02100	Aaw02100 Human neu
36	710.5	36.2	307	2	AAR97196	Aar97196 Mouse neu
37	705.5	35.9	301	2	AAR48751	Aar48751 G-protein
38	705.5	35.9	301	2	AAW02723	Aaw02723 G-protein
39	573	29.2	290	4	AAE06693	Aae06693 Human neu
40	573	29.2	290	6	ABP81945	Abp81945 Human neu
41	561.5	28.6	383	4	AAE08015	Aae08015 Pig chime
42	560.5	28.5	383	4	AAE08009	Aae08009 Dog chime
43	557	28.3	395	4	AAE08013	Aae08013 Rat chime
44	556.5	28.3	394	4	AAE08005	Aae08005 Human chi
45	556.5	28.3	394	5	ABB79512	Abb79512 Chimeric

ALIGNMENTS

RESULT 1
AAE06691
ID AAE06691 standard; protein; 375 AA.
XX
AC AAE06691;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human neuropeptide Y (NPY) Y4 receptor.
XX
KW Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;
KW cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
KW fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
KW osteopenia; bone metastasis; neurotransmitter; osteogenic;
KW NPY Y4 receptor.
XX
OS Homo sapiens.
XX
PN WO200153477-A1.
XX
PD 26-JUL-2001.
XX
PF 22-JAN-2001; 2001WO-US002040.
XX
PR 20-JAN-2000; 2000US-00489872.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMLI/) AMLING M.
XX
PI Amling M, Karsenty G, Ducy P;
XX
DR WPI; 2001-488709/53.
DR N-PSDB; AAD12802.
XX
PT Treating or preventing reduced bone mass, e.g. osteoporosis, by reducing
PT the level of neuropeptide Y activity in blood or cerebrospinal fluid.
XX
PS Example 7; Page 86; 102pp; English.
XX
CC The present invention relates to a method for treatment or prevention of
CC bone diseases characterised by loss of bone mass, comprises administering
CC to a mammal a compound that lowers the level of neuropeptide Y (NPY) in
CC the serum or cerebrospinal fluid (CSF) or a compound that lowers the
CC level of inositol phosphate (IP) or extracellular signal-regulated kinase
CC (ERK). The method is specifically used to treat (including by gene
CC therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may
CC also be used e.g., in cases of fractures or bone metastases. These
CC diseases may also be diagnosed by detecting elevated NPY levels,

```
CC   including monitoring of treatment, assessing efficacy of compounds in
CC   clinical trials and for identifying subjects at risk. The present
CC   sequence is a human NPY Y4 receptor
XX
SQ   Sequence 375 AA;

  Query Match             100.0%;  Score 1965;  DB 4;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-193;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
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Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
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Db        361 VSKGSLRLSGRSNPI 375


RESULT 2
ABB84501
ID   ABB84501 standard; protein; 375 AA.
XX
AC   ABB84501;
XX
DT   20-DEC-2002  (first entry)
XX
DE   Human hippocampus Y4 receptor protein.
XX
KW   Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor;
KW   food consumption; metabolic; anorectic; antidepressant; tranquiliser;
KW   antimigraine; analgesic; hypotensive; cerebroprotective; cardiant;
KW   antidiarrhoeic; haemostatic; vaccine; anorexia; obesity; bulimia;
KW   sexual disorder; reproductive disorder; depression; anxiety; memory loss;
KW   migraine; pain; epileptic seizure; hypertension; cerebral haemorrhage;
KW   shock; congestive heart failure; sleeve disturbance; nasal congestion;
KW   diarrhoea; Y4.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          41. .67
FT                   /label= transmembrane_domain_I
FT   Domain          78. .100
FT                   /label= transmembrane_domain_II
FT   Domain          116. .137
FT                   /label= transmembrane_domain_III
FT   Domain          155. .177
FT                   /label= transmembrane_domain_IV
FT   Domain          213. .235
FT                   /label= transmembrane_domain_V
FT   Domain          267. .290
FT                   /label= transmembrane_domain_VI
FT   Domain          303. .325
FT                   /label= transmembrane_domain_VII
XX
PN   US2002103123-A1.
XX
PD   01-AUG-2002.
XX
PF   24-SEP-2001; 2001US-00962646.
XX
PR   02-DEC-1994;   94US-00349025.
PR   01-DEC-1995;   95US-00566096.
PR   25-NOV-1998;   98US-00200673.
XX
PA   (SYNA-) SYNAPTIC PHARM CORP.
XX
PI   Gerald CPG,  Weinshank RL,  Walker MW,  Branchek T;
XX
DR   WPI; 2002-712388/77.
XX
PT   Modifying feeding behavior of subject, useful in treating feeding
PT   disorders, involves administering to subject Y5 receptor agonist or
PT   antagonist, to increase or decrease consumption of food by subject.
XX
PS   Disclosure; Fig 8A-C; 102pp; English.
XX
CC   This invention describes a novel method of modifying feeding behaviour of
CC   a subject which involves administering to the subject an amount of a
CC   compound which is a Y5 receptor agonist or antagonist effective to
CC   increase or decrease, respectively, the consumption of food by the
CC   subject so as to modify feeding behaviour of the subject. The product of
CC   the invention has metabolic, anorectic, antidepressant, tranquiliser,
CC   antimigraine, analgesic, hypotensive, cerebroprotective, cardiant,
CC   antidiarrhoeic and haemostatic activity and can be used in a vaccine. Y5
CC   receptor agonist or antagonist compounds are useful for treating a
CC   feeding disorder (e.g. anorexia, obesity or bulimia) in a subject. The
CC   pharmaceutical compositions described in the disclosure are useful for
CC   treating an abnormality alleviated by the inhibition or activation of Y5
CC   receptor, in a subject. Antibodies raised against the receptor are useful
CC   for detecting the presence of the receptor on the surface of a cell. The
CC   agonist of Y5 receptor is useful for treating an abnormality in a
CC   subject, where the abnormality includes anorexia, sexual/reproductive
CC   disorder, depression, anxiety, memory loss, migraine, pain, epileptic
CC   seizure, hypertension, cerebral haemorrhage, shock, congestive heart
CC   failure, sleeve disturbance, nasal congestion, and diarrhoea. This
CC   sequence represents the human hippocampus Y4 receptor described in the
CC   disclosure of the invention
XX
SQ   Sequence 375 AA;

  Query Match             100.0%;  Score 1965;  DB 5;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-193;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
```

```
Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375
```

RESULT 3
ABP81859
ID ABP81859 standard; protein; 375 AA.
XX
AC ABP81859;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human neuropeptide Y receptor type 4 protein SEQ ID NO:203.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42706.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 1965; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.3e-193;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAPI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375
```

RESULT 4
AAR79119
ID AAR79119 standard; protein; 375 AA.
XX
AC AAR79119;
XX
DT 07-DEC-1995 (first entry)
XX
DE Neuropeptide Y/peptide YY/pancretic polypeptide receptor (Y4).
XX
KW Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;
KW therapeutic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 39. .66
FT /note= "transmembrane spanning region I"
FT Region 78. .104
FT /note= "transmembrane spanning region II"
FT Region 118. .137
FT /note= "transmembrane spanning region III"
FT Region 156. .178
FT /note= "transmembrane spanning region IV"
FT Region 212. .235
FT /note= "transmembrane spanning region V"
FT Region 263. .288
FT /note= "transmembrane spanning region VI"
FT Region 302. .326
FT /note= "transmembrane spanning region VII"

XX
PN WO9517906-A1.
XX
PD 06-JUL-1995.
XX
PF 28-DEC-1994; 94WO-US014436.
XX
PR 28-DEC-1993; 93US-00176412.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Bard JA, Walker MW, Branchek T, Weinshank RL;
XX
DR WPI; 1995-246190/32.
DR N-PSDB; AAQ94171.
XX
PT New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -
PT useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc.
XX
PS Disclosure; Fig 1; 154pp; English.
XX
CC The sequence represents a human neuropeptide Y/peptide YY/ pncretic
CC polypeptide (Y4) receptor, which can be used to screen drugs which bind
CC to it, specifically to find ligands (agonists or antagonists) which bind
CC to it. The ligands can be used to treat abnormalities, specifically the
CC antagonists can be used to treat amnesia, feeding disorders, epilepsy,
CC hypertension, sleeping disorders or pain
XX
SQ Sequence 375 AA;

Query Match 99.5%; Score 1956; DB 2; Length 375;
Best Local Similarity 99.5%; Pred. No. 6.1e-192;
Matches 373; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||| :|||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGERVCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375
```

RESULT 5
ABG73516
ID ABG73516 standard; protein; 375 AA.
XX
AC ABG73516;
XX
DT 14-FEB-2003 (first entry)
XX
DE Murine NY4R protein SEQ ID 47.
XX

KW G-protein coupled receptor; HGPRBMY1; HGPRBMY2; immunosuppressive;
KW cardiant; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KW vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW birth defect; aberrant phosphorylation; acute phase response; receptor;
KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW necrotic lesion; wound; organ transplant rejection.
XX
OS Mus musculus.
XX
PN WO200268591-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005281.
XX
PR 23-FEB-2001; 2001US-0270792P.
PR 23-FEB-2001; 2001US-0270793P.
PR 06-JUN-2001; 2001US-0296427P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
DR WPI; 2003-058304/05.
XX
PT New human HGPRBMY1 or HGPRBMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.
XX
PS Disclosure; Fig 9; 316pp; English.
XX
CC This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGPRBMY1 or HGPRBMY2 which have immunosuppressive, cardiant,
CC neuroprotective, antiinflammatory, cytostatic and vulnerary activity and
CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC comprising HGPRBMY1 or HGPRBMY2 polypeptides or their agonists or
CC antagonists or modulators, or a HGPRBMY1- or HGPRBMY2-specific antibody
CC are useful for preventing, treating or ameliorating a medical condition
CC comprising autoimmune, cardiovascular, neural, reproductive,
CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC cell cycle or birth defect, a disorder related to aberrant
CC phosphorylation, acute phase responses or signal transduction or to
CC hyperimmune activity, an inflammatory or hypercongenital condition, a
CC necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence represents a G-
CC protein coupled receptor associated with the human HGPRBMY proteins
CC described in the disclosure of the invention
XX
SQ Sequence 375 AA;

Query Match 77.3%; Score 1519; DB 6; Length 375;
Best Local Similarity 75.9%; Pred. No. 4.5e-147;
Matches 283; Conservative 35; Mismatches 55; Indels 0; Gaps 0;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||| || | | | ||:| : || :|||||: |||| ::: ||:|:||||||::||||||
Db          1 MNTSHFLAPLFPGSLQGKNGTNPLDSPYNFSDGCQDSAELLAFIITTYSIETILGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:||||||||||||||||||:|||||  |||||||||| |||| ||
Db         61 CLIPVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||||||||| |||||||:|| |:| ||||||||| |
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSIFQAYLGIVVIWFISCFLSLPFLANSTL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ::|| |||| :||| ||||| || ||| ||||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCIPLAFILVCYIRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
```

```
Db        241 LQRQKHVFHAHACSSRAGQMKRINSMLMTMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:|||||||||||||||||||| ||||:||||||||    :|  ||||||||||||:
Db        301 NLIFLMCHLLAMASTCVNPFIYGFLNINFKKDIKALVLTCHCRSPQGESEHLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373
```

RESULT 6
AAR79120
ID AAR79120 standard; protein; 375 AA.
XX
AC AAR79120;
XX
DT 09-DEC-1995 (first entry)
XX
DE Neuropeptide Y/peptide YY/pancretic polypeptide receptor (Y4).
XX
KW Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;
KW therapeutic.
XX
OS Rattus rattus.
XX

FH	Key	Location/Qualifiers
FT	Region	39. .66
FT		/note= "transmembrane spanning region I"
FT	Region	78. .104
FT		/note= "transmembrane spanning region II"
FT	Region	118. .137
FT		/note= "transmembrane spanning region III"
FT	Region	156. .178
FT		/note= "transmembrane spanning region IV"
FT	Region	212. .235
FT		/note= "transmembrane spanning region V"
FT	Region	263. .288
FT		/note= "transmembrane spanning region VI"
FT	Region	302. .326
FT		/note= "transmembrane spanning region VII"

XX
PN WO9517906-A1.
XX
PD 06-JUL-1995.
XX
PF 28-DEC-1994; 94WO-US014436.
XX
PR 28-DEC-1993; 93US-00176412.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Bard JA, Walker MW, Branchek T, Weinshank RL;
XX
DR WPI; 1995-246190/32.
DR N-PSDB; AAQ94172.
XX
PT New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -
PT useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc.
XX
PS Disclosure; Fig 3; 154pp; English.
XX
CC The sequence represents a rat neuropeptide Y/peptide YY/ pncretic
CC polypeptide (Y4) receptor, which can be used to screen drugs which bind
CC to it, specifically to find ligands (agonists or antagonists) which bind
CC to it. The ligands can be used to treat abnormalities, specifically the
CC antagonists can be used to treat amnesia, feeding disorders, epilepsy,
CC hypertension, sleeping disorders or pain
XX
SQ Sequence 375 AA;

Query Match 76.0%; Score 1494; DB 2; Length 375;
Best Local Similarity 75.1%; Pred. No. 1.7e-144;
Matches 280; Conservative 35; Mismatches 58; Indels 0; Gaps 0;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||:| | |    ||:| : || : || |: |||| |:: ||:|:||:||||:||||||
Db          1 MNTSHLMASLSPAFLQGKNGTNPLDSLYNLSDGCQDSADLLAFIITTYSVETVLGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:||||||||||||||||||:|||||  |||||||||| |||| ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||:|| |:| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVVIWFISCFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ::|| |||| :||| ||||| || ||| ||||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCVPLAFILVCYMRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| | ||  | | | | ||::| :|: || ||||||||||||:||||: |||| |||
Db        241 LQRQRRAFHTHTCSSRVGQMKRINGMLMAMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:||| |||||||||||||||| ||||:||||||||:   | | | ||||||||:
Db        301 NLIFLMCHLFAMASTCVNPFIYGFLNINFKKDIKALVLTCRCRPPQGEPEPLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373
```

RESULT 7
ABG73517
ID ABG73517 standard; protein; 375 AA.
XX
AC ABG73517;
XX
DT 14-FEB-2003 (first entry)
XX
DE Rat NY4R protein SEQ ID 48.
XX
KW G-protein coupled receptor; HGPRBMY1; HGPRBMY2; immunosuppressive;
KW cardiant; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KW vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW birth defect; aberrant phosphorylation; acute phase response; receptor;
KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW necrotic lesion; wound; organ transplant rejection.
XX
OS Rattus sp.
XX
PN WO200268591-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005281.
XX
PR 23-FEB-2001; 2001US-0270792P.
PR 23-FEB-2001; 2001US-0270793P.
PR 06-JUN-2001; 2001US-0296427P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
DR WPI; 2003-058304/05.
XX
PT New human HGPRBMY1 or HGPRBMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.
XX

PS Disclosure; Fig 9; 316pp; English.
XX
CC This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGPRBMY1 or HGPRBMY2 which have immunosuppressive, cardiant,
CC neuroprotective, antiinflammatory, cytostatic and vulnerary activity and
CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC comprising HGPRBMY1 or HGPRBMY2 polypeptides or their agonists or
CC antagonists or modulators, or a HGPRBMY1- or HGPRBMY2-specific antibody
CC are useful for preventing, treating or ameliorating a medical condition
CC comprising autoimmune, cardiovascular, neural, reproductive,
CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC cell cycle or birth defect, a disorder related to aberrant
CC phosphorylation, acute phase responses or signal transduction or to
CC hyperimmune activity, an inflammatory or hypercongenital condition, a
CC necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence represents a G-
CC protein coupled receptor associated with the human HGPRBMY proteins
CC described in the disclosure of the invention
XX
SQ Sequence 375 AA;

Query Match 76.0%; Score 1494; DB 6; Length 375;
Best Local Similarity 75.1%; Pred. No. 1.7e-144;
Matches 280; Conservative 35; Mismatches 58; Indels 0; Gaps 0;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              |||||:| | |  ||:| : || : || |: |||| |:: ||:|:||:|||:|||||
Db          1 MNTSHLMASLSPAFLQGKNGTNPLDSLYNLSDGCQDSADLLAFIITTYSVETVLGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:|||||||||||||||||||:|||||  |||||||||| |||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||:|| |:| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVVIWFISCFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| ||||| || ||| ||||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCVPLAFILVCYMRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| | ||  | | | | ||::| :|: || |||||||||||||:|||||: |||| |||
Db        241 LQRQRRAFHTHTCSSRVGQMKRINGMLMAMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:||| |||||||||||||||| ||||:||||||||:   | | | |||||||||:
Db        301 NLIFLMCHLFAMASTCVNPFIYGFLNININFKKDIKALVLTCRCRPPQGEPEPLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373
```

RESULT 8
ABG73520
ID ABG73520 standard; protein; 375 AA.
XX
AC ABG73520;
XX
DT 14-FEB-2003 (first entry)
XX
DE D. rerio G-protein coupled receptor SEQ ID 51.
XX
KW G-protein coupled receptor; HGPRBMY1; HGPRBMY2; immunosuppressive;
KW cardiant; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KW vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW birth defect; aberrant phosphorylation; acute phase response; receptor;
KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW necrotic lesion; wound; organ transplant rejection.
XX
OS Danio rerio.

XX
PN WO200268591-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005281.
XX
PR 23-FEB-2001; 2001US-0270792P.
PR 23-FEB-2001; 2001US-0270793P.
PR 06-JUN-2001; 2001US-0296427P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
DR WPI; 2003-058304/05.
XX
PT New human HGPRBMY1 or HGPRBMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.
XX
PS Disclosure; Fig 9; 316pp; English.
XX
CC This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGPRBMY1 or HGPRBMY2 which have immunosuppressive, cardiant,
CC neuroprotective, antiinflammatory, cytostatic and vulnerary activity and
CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC comprising HGPRBMY1 or HGPRBMY2 polypeptides or their agonists or
CC antagonists or modulators, or a HGPRBMY1- or HGPRBMY2-specific antibody
CC are useful for preventing, treating or ameliorating a medical condition
CC comprising autoimmune, cardiovascular, neural, reproductive,
CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC cell cycle or birth defect, a disorder related to aberrant
CC phosphorylation, acute phase responses or signal transduction or to
CC hyperimmune activity, an inflammatory or hypercongenital condition, a
CC necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence represents a G-
CC protein coupled receptor associated with the human HGPRBMY proteins
CC described in the disclosure of the invention
XX
SQ Sequence 375 AA;

Query Match 48.9%; Score 960; DB 6; Length 375;
Best Local Similarity 50.1%; Pred. No. 1.1e-89;
Matches 188; Conservative 57; Mismatches 112; Indels 18; Gaps 3;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              | |||           | | | |     |  |:  :|:: :||   ||::||
Db          1 MERSHL-----------NNSSWLLEDP-----TCPASLSSTTFLIVAYSTMLAVGLVGNT 44

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: |  ||||  ||||: | ||: || |:||:| |:| :|||:|| || || |||:: |:
Db         45 CLVVVITRQKEMRNVTNIFIVNLSCSDILVCLVCLPVTIIYTLMDRWILGEALCKVTPFV 104

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||  |:||:||||||||:|||||  :  :|| : :||:|||  :|||||: :||
Db        105 QCMSVTVSIFSMVLIALERHQLIIHPTGWKPVVRHSYLAVAVIWIIACFISLPFLSFNIL 164

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              |    | |      :|  :| | ||   :|  ||| ||| ||||||  ||||| ||: |
Db        165 TNSPFHNLSLPFNPFSDHFICIEQWPSEGNRLTYTTTLLLCQYCLPLALILVCYFRIFLR 224

Qy        241 LQRQGRVFH--KGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPIC 298
              | |:  :   :|    :|    |:|| :|  :| |||: ||||:|||:: ||:|||||:|
Db        225 LSRRKDMVERARGGRQKKAKGSKRVNAMLASIVAAFALCWLPLNVFNTIFDWNHEAIPVC 284

Qy        299 HGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVH 358
              : ||  ||| |||||||| |||||| ||:||:|:|:  |:   | |  |  |||||
Db        285 QHDAIFSACHLTAMASTCVNPVIYGFLNNNFQKELKSLLSRCRCWGPAESYESFPLSTVS 344

Qy        359 TEVSKGSLRLSGRSN 373
              | ::|||:  :| ::
```

```
Db        345 TGITKGSILSNGSAS 359


RESULT 9
AAE08001
ID   AAE08001 standard; protein; 382 AA.
XX
AC   AAE08001;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Rat neuropeptide Y1 (NPY1) receptor.
XX
KW   Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KW   transmembrane; TM domain; therapy; obesity; blood pressure; eiplepsy;
KW   Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW   locomotor; anxiety disorder; limbic seizure; tranquilliser; rat.
XX
OS   Rattus norvegicus.
XX
FH   Key             Location/Qualifiers
FT   Domain          231. .262
FT                   /note= "Third intracellular loop domain"
XX
PN   WO200155103-A2.
XX
PD   02-AUG-2001.
XX
PF   29-JAN-2001; 2001WO-US002804.
XX
PR   28-JAN-2000; 2000US-0178652P.
XX
PA   (NEUR-) NEUROGEN CORP.
XX
PI   Bennett M,  Brodbeck R,  Krause J;
XX
DR   WPI; 2001-514543/56.
XX
PT   New chimeric receptor proteins comprising a single polypeptide chain of
PT   amino acids, useful as targets for drug actions, and as basis for drug
PT   discovery and development.
XX
PS   Disclosure; Page 46-47; 72pp; English.
XX
CC   The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC   The NPY receptors are G-protein-coupled transmembrane proteins with seven
CC   membrane spanning transmembrane (TM) domains. The compounds that modulate
CC   the activity of a NPY receptor is useful in the preparation of a
CC   medicament for treating conditions including obesity, high/low blood
CC   pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC   seizure, locomotor and anxiety disorders. They can also be used as
CC   targets for drug actions, and as basis for drug discovery and
CC   development. The NPY5 receptor may have an anti-epileptic activity in the
CC   control of limbic seizures. The present sequence is rat NPY1 receptor
XX
SQ   Sequence 382 AA;

  Query Match             44.2%;  Score 869;  DB 4;  Length 382;
  Best Local Similarity   46.8%;  Pred. No. 2.5e-80;
  Matches  168;  Conservative   74;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:          |   : |:  :  :|     ::|| ||| |: : ::|||  ||||
Db         16 YNVSENSPFLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              |||||||| ||:|:   ||:|| :|||:|   ||||:   || :   :| |  |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:  :  |   |  |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::||:|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| || |||
Db        254 SSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFFLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::     |   :  :: | : :||:|||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 10
ABG73519
ID   ABG73519 standard; protein; 383 AA.
XX
AC   ABG73519;
XX
DT   14-FEB-2003  (first entry)
XX
DE   C. porcellus G-protein coupled receptor SEQ ID 50.
XX
KW   G-protein coupled receptor; HGPRBMY1; HGPRBMY2; immunosuppressive;
KW   cardiant; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KW   vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
KW   haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW   birth defect; aberrant phosphorylation; acute phase response; receptor;
KW   signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW   necrotic lesion; wound; organ transplant rejection.
XX
OS   Cavea porcellus.
XX
PN   WO200268591-A2.
XX
PD   06-SEP-2002.
XX
PF   22-FEB-2002; 2002WO-US005281.
XX
PR   23-FEB-2001; 2001US-0270792P.
PR   23-FEB-2001; 2001US-0270793P.
PR   06-JUN-2001; 2001US-0296427P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Feder J,  Ramanathan C,  Nelson T,  Mintier G,  Cacace A,  Barber L;
PI   Kornacker M,  Bol D;
XX
DR   WPI; 2003-058304/05.
XX
PT   New human HGPRBMY1 or HGPRBMY2 polynucleotide and polypeptide, useful
PT   preventing, treating or ameliorating a disorder e.g., wound,
PT   cardiovascular disorder or transplant rejection.
XX
PS   Disclosure; Fig 9; 316pp; English.
XX
CC   This invention describes the novel human G-protein coupled receptors
CC   (GPCR's), HGPRBMY1 or HGPRBMY2 which have immunosuppressive, cardiant,
CC   neuroprotective, antiinflammatory, cytostatic and vulnerary activity and
CC   can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC   comprising HGPRBMY1 or HGPRBMY2 polypeptides or their agonists or
CC   antagonists or modulators, or a HGPRBMY1- or HGPRBMY2-specific antibody
CC   are useful for preventing, treating or ameliorating a medical condition
CC   comprising autoimmune, cardiovascular, neural, reproductive,
CC   haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC   cell cycle or birth defect, a disorder related to aberrant
CC   phosphorylation, acute phase responses or signal transduction or to
CC   hyperimmune activity, an inflammatory or hypercongenital condition, a
CC   necrotic lesion, a wound, organ transplant rejection or a condition
CC   related to organ transplant rejection. This sequence represents a G-
CC   protein coupled receptor associated with the human HGPRBMY proteins
CC   described in the disclosure of the invention
XX
```

```
SQ   Sequence 383 AA;

  Query Match             44.1%;  Score 867.5;  DB 6;  Length 383;
  Best Local Similarity   45.4%;  Pred. No. 3.6e-80;
  Matches  169;  Conservative   76;  Mismatches  106;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSEH-----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
                | || |      || ||           |   : |:  :  :|    ::|| ||| |:
Db          8 QLENHS----VHYNLSEEKPSFFAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIL 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:||||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWIFGEIMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||||| ||:|:   ||:|| :|||:|   ||||:   :| :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYIGIAVIWVLAVASSLPFMIYQVLTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
               :|     |:   ||:|| : :|    ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAFKDKLVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHKGTYS-LRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |   |  |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDSKYRSSESKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| |||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
               ||:   :::|:
Db        362 TSLK---QASPL 370


RESULT 11
AAW02101
ID   AAW02101 standard; protein; 382 AA.
XX
AC   AAW02101;
XX
DT   25-OCT-1996  (first entry)
XX
DE   Mouse neuropeptide Y1 receptor.
XX
KW   Neuropeptide Y1 receptor; NPY Yx; G-protéin coupled receptor; obesity;
KW   diabetes; cardiac vasospasm; Parkinson's disease.
XX
OS   Mus sp.
XX
PN   WO9623809-A1.
XX
PD   08-AUG-1996.
XX
PF   30-JAN-1996;   96WO-US001444.
XX
PR   03-FEB-1995;   95US-00383746.
PR   03-APR-1995;   95US-00415818.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Cascieri MA,  Linemeyer DL,  Macneil DJ,  Shiao L,  Strader C;
PI   Weinberg DH,  Tan CP;
XX
DR   WPI; 1996-371369/37.
XX
PT   DNA mol. encoding neuro:peptide Y Yx receptor - useful in assays to
PT   identify cpds. which bind to receptor, useful to treat, e.g. obesity,
PT   diabetes, cardiac vasospasm and Parkinson's disease.
XX
PS   Disclosure; Page 50-52; 65pp; English.
XX
CC   Mouse neuropeptide Y1 receptor (AAW02101) is stimulated by NPY and
CC   peptide YY and appears to be a major vascular receptor. It has been
CC   cloned and shown to be a G-protein coupled receptor. A DNA sequence
CC   encoding NPY Y1 receptor was used to design PCR primers (AAT36129-32)
CC   that were utilised in the construction of probes used to screen a mouse
CC   genomic library. This led to the isolation of a DNA fragment (AAT36127)
CC   coding for a novel NPY receptor subtype, NPY Yx receptor (AAW02099)
XX
SQ   Sequence 382 AA;

  Query Match             44.1%;  Score 867;  DB 2;  Length 382;
  Best Local Similarity   46.5%;  Pred. No. 4e-80;
  Matches  167;  Conservative   75;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:           |   : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db         16 YNASENSPLLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              |||||||| ||:|:   ||:|| :|||:|   ||||:   || :   :| | |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:  :  |   |  |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:|||:||| || |||
Db        254 SSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::     |   :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 12
AAW02099
ID   AAW02099 standard; protein; 371 AA.
XX
AC   AAW02099;
XX
DT   25-OCT-1996  (first entry)
XX
DE   Mouse neuropeptide Y Yx receptor.
XX
KW   Neuropeptide Y Yx receptor; NPY Yx; G-protein coupled receptor; obesity;
KW   diabetes; cardiac vasospasm; Parkinson's disease.
XX
OS   Mus sp.
XX
PN   WO9623809-A1.
XX
PD   08-AUG-1996.
XX
PF   30-JAN-1996;   96WO-US001444.
XX
PR   03-FEB-1995;   95US-00383746.
PR   03-APR-1995;   95US-00415818.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Cascieri MA,  Linemeyer DL,  Macneil DJ,  Shiao L,  Strader C;
PI   Weinberg DH,  Tan CP;
XX
DR   WPI; 1996-371369/37.
DR   N-PSDB; AAT36127.
XX
PT   DNA mol. encoding neuro:peptide Y Yx receptor - useful in assays to
PT   identify cpds. which bind to receptor, useful to treat, e.g. obesity,
PT   diabetes, cardiac vasospasm and Parkinson's disease.
```

XX
PS Claim 38; Page 49-50; 65pp; English.
XX
CC Mouse neuropeptide Y Yx (NPY Yx) receptor (AAW02099), a novel subtype of
CC NPY, is a G-protein coupled receptor having 7 transmembrane-spanning
CC domains. Its amino acid sequence was deduced from a genomic DNA fragment
CC (AAT36127) obtd. from a mouse cosmid library. Vectors were constructed to
CC allow expression of the murine NPY Yx receptor in mammalian (COS-7)
CC cells. The recombinant receptor, or transformed host cells, can be used
CC to screen for cpds. that modulate the function of the receptor, or
CC modulate the expression of nucleic acids encoding the receptor. Such
CC cpds. are useful for treating a variety of disease conditions
XX
SQ Sequence 371 AA;

Query Match 43.9%; Score 863; DB 2; Length 371;
Best Local Similarity 43.2%; Pred. No. 9.9e-80;
Matches 156; Conservative 89; Mismatches 108; Indels 8; Gaps 5;

Qy 12 PKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTV-RQK 70
Db 10 PNKTSGKSNN----SAFFYFESCQPPFLAILLLLIAYTVILIMGIFGNLSLIIIIFKKQR 65

Qy 71 EKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSIL 130
Db 66 EAQNVTNILIANLSLSDILVCVMCIPFTVIYTLMDHWVFGNTMCKLTSYVQSVSVSVSIF 125

Qy 131 SLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLP-FLANSILENVFHKNHS 189
Db 126 SLVLIAIERYQLIVNPRGWKPRVAHAYWGIILIWLISLTLSIPLFLSYHLTNEPFH-NLS 184

Qy 190 KALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGR-VF 248
Db 185 LPTDIYTHQVACVEIWPSKLNQLLFSTSLFMLQYFVPLGFILICYLKIVLCLRKRTRQVD 244

Qy 249 HKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCH 308
Db 245 RRKENKSRLNENKRVNVMLISIVVTFGACWLPLNIFNVIFDWYHEMLMSCHHDLVFVVCH 304

Qy 309 LLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRL 368
Db 305 LIAMVSTCINPLFYGFLNKNFQKDLMMLIHHCWCGEPQESYENIAMSTMHTDESKGSLKL 364

Qy 369 S 369
Db 365 A 365

RESULT 13
ABB84499
ID ABB84499 standard; protein; 384 AA.
XX
AC ABB84499;
XX
DT 20-DEC-2002 (first entry)
XX
DE Human hippocampus Y1 receptor protein.
XX
KW Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor;
KW food consumption; metabolic; anorectic; antidepressant; tranquiliser;
KW antimigraine; analgesic; hypotensive; cerebroprotective; cardiant;
KW antidiarrhoeic; haemostatic; vaccine; anorexia; obesity; bulimia;
KW sexual disorder; reproductive disorder; depression; anxiety; memory loss;
KW migraine; pain; epileptic seizure; hypertension; cerebral haemorrhage;
KW shock; congestive heart failure; sleeve disturbance; nasal congestion;
KW diarrhoea; Y1.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 40. .66
FT /label= transmembrane_domain_I
FT Domain 77. .99
FT /label= transmembrane_domain_II
FT Domain 115. .136
FT /label= transmembrane_domain_III
FT Domain 155. .177
FT /label= transmembrane_domain_IV
FT Domain 210. .232
FT /label= transmembrane_domain_V
FT Domain 265. .288
FT /label= transmembrane_domain_VI
FT Domain 301. .323
FT /label= transmembrane_domain_VII
XX
PN US2002103123-A1.
XX
PD 01-AUG-2002.
XX
PF 24-SEP-2001; 2001US-00962646.
XX
PR 02-DEC-1994; 94US-00349025.
PR 01-DEC-1995; 95US-00566096.
PR 25-NOV-1998; 98US-00200673.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Gerald CPG, Weinshank RL, Walker MW, Branchek T;
XX
DR WPI; 2002-712388/77.
XX
PT Modifying feeding behavior of subject, useful in treating feeding
PT disorders, involves administering to subject Y5 receptor agonist or
PT antagonist, to increase or decrease consumption of food by subject.
XX
PS Disclosure; Fig 8A-C; 102pp; English.
XX
CC This invention describes a novel method of modifying feeding behaviour of
CC a subject which involves administering to the subject an amount of a
CC compound which is a Y5 receptor agonist or antagonist effective to
CC increase or decrease, respectively, the consumption of food by the
CC subject so as to modify feeding behaviour of the subject. The product of
CC the invention has metabolic, anorectic, antidepressant, tranquiliser,
CC antimigraine, analgesic, hypotensive, cerebroprotective, cardiant,
CC antidiarrhoeic and haemostatic activity and can be used in a vaccine. Y5
CC receptor agonist or antagonist compounds are useful for treating a
CC feeding disorder (e.g. anorexia, obesity or bulimia) in a subject. The
CC pharmaceutical compositions described in the disclosure are useful for
CC treating an abnormality alleviated by the inhibition or activation of Y5
CC receptor, in a subject. Antibodies raised against the receptor are useful
CC for detecting the presence of the receptor on the surface of a cell. The
CC agonist of Y5 receptor is useful for treating an abnormality in a
CC subject, where the abnormality includes anorexia, sexual/reproductive
CC disorder, depression, anxiety, memory loss, migraine, pain, epileptic
CC seizure, hypertension, cerebral haemorrhage, shock, congestive heart
CC failure, sleeve disturbance, nasal congestion, and diarrhoea. This
CC sequence represents the human hippocampus Y1 receptor described in the
CC disclosure of the invention
XX
SQ Sequence 384 AA;

Query Match 43.8%; Score 860.5; DB 5; Length 384;
Best Local Similarity 44.9%; Pred. No. 1.9e-79;
Matches 167; Conservative 77; Mismatches 107; Indels 21; Gaps 5;

Qy 16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
Db 8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy 65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
Db 64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPLTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy 125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
Db 124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

```
Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|    |:    || || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
                : |       |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| |||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
                ||:   :::|:
Db        362 TSLK---QASPV 370
```

RESULT 14
AAB14324
ID AAB14324 standard; protein; 383 AA.
XX
AC AAB14324;
XX
DT 22-NOV-2000 (first entry)
XX
DE Rhesus Y1 receptor.
XX
KW Rhesus monkey; Y1 receptor; neuropeptide Y; neurotransmitter; vasospasm;
KW heart failure, shock; cardiac hypertrophy; high blood pressure; angina;
KW myocardial infarction; sudden cardiac death; arrhythmia; renal failure;
KW peripheral vascular disease.
XX
OS Macaca mulatta.
XX
PN US6087154-A.
XX
PD 11-JUL-2000.
XX
PF 20-MAR-1998; 98US-00045186.
XX
PR 21-MAR-1997; 97US-0041177P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Baez M, George CA;
XX
DR WPI; 2000-523725/47.
DR N-PSDB; AAA62587, AAA62588.
XX
PT Nucleic acid compound for identifying compounds for treating conditions
PT associated with excess or deficiency of neuropeptide Y encodes rhesus Y1
PT receptor which has affinity for neuropeptide Y and related peptides.
XX
PS Claim 2; Col 33-34; 21pp; English.
XX
CC The present sequence is the rhesus Y1 receptor, which has affinity for
CC neuropeptide Y, pancreatic peptide and peptide YY. Neuropeptide Y is a
CC peptide present in the central and peripheral nervous systems. The
CC peptide coexists with noradrenaline in many neurons and acts as a
CC neurotransmitter alone or synergistically together with noradrenaline.
CC Neuropeptide Y interacts with a family of closely related receptors. The
CC Y1 receptor subtype appears to be the major vascular neuropeptide Y
CC receptor. The rhesus Y1 recptor is useful in identifying compounds for
CC treatment or prevention of conditions associated with an excess or
CC deficiency of neuropeptide Y. Such disorders include vasospasm, heart
CC failure, shock, cardiac hypertrophy, increased blood pressure, angina,
CC myocardial infarction, sudden cardiac death, arrhythmia, peripheral
CC vascular disease, and abnormal renal conditions such as impaired flow of
CC fluid, abnormal mass transport, or renal failure
XX
SQ Sequence 383 AA;

```
  Query Match           43.6%;  Score 856.5;  DB 3;  Length 383;
  Best Local Similarity  44.6%;  Pred. No. 4.8e-79;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||            |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|    |:   || || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
                : |       |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| |||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
                ||:   :::|:
Db        362 TSLK---QASPV 370
```

RESULT 15
AAR35493
ID AAR35493 standard; protein; 384 AA.
XX
AC AAR35493;
XX
DT 25-MAR-2003 (revised)
DT 06-SEP-1993 (first entry)
XX
DE Human NPY receptor subtype Y1.
XX
KW PCR; domain; primer; human; brain; neuropeptide; Y; NPY-Y1; receptor;
KW isolation; clone; fetal; NPY; probe; adult; hippocampus; cDNA library;
KW subtype Y1; cytoplasmic loop; kC; transmembrane; G protein; rat.
XX
OS Homo sapiens.
XX
PN WO9309227-A1.
XX
PD 13-MAY-1993.
XX
PF 06-NOV-1992; 92WO-AU000600.
XX
PR 06-NOV-1991; 91AU-00009336.
PR 23-JUN-1992; 92AU-00003131.
XX
PA (GARV-) GARVAN INST MEDICAL RES.
XX
PI Selbie L, Herzog H, Shine J;
XX
DR WPI; 1993-167694/20.
DR N-PSDB; AAQ40768.
XX
PT Human neuro-peptide Y-Y1 receptor and its DNA - useful for screening for
PT NPY agonists or antagonists.
XX
PS Disclosure; Page 8-10; 32pp; English.
XX
CC This sequence represents the human neuropeptide Y (NPY) receptor subtype
CC Y1. The cDNA encoding this sequence was isolated from human fetal brain

CC and human adult hippocampus cDNA libraries, using the primers given in
CC AAQ40766-67 which correspond to position 672-584 and 48-78 in the rat
CC cDNA clone FC5R, respectively. The longest isolated clone encoded the
CC human NPY receptor subtype Y1. This clone was used to probe a human
CC genomic library which lead to the isolation of the clone kC (see also
CC AAR35494) which contains the NPY Y1 receptor gene. The human NPY Y1
CC receptor consists of 3 exons and covers approx. 10 kb. The first 57
CC nucleotides of the 5' untranslated sequence of the human hippocampal NPY
CC Y1 receptor mRNA are separated by a 6 kb intron from the second exon. The
CC second intron containing an in frame stop codon, is located exactly after
CC the fifth transmembrane domain at nucleotide 908 of the cDNA sequence.
CC The third cytoplasmic loop of the receptor is thought to form a specific
CC domain involved in determination of the specificity of coupling to
CC different G proteins. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 384 AA;

Query Match 43.6%; Score 856.5; DB 2; Length 384;
Best Local Similarity 44.6%; Pred. No. 4.8e-79;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;

```
Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
Db        362 TSLK---QASPV 370
```

Search completed: May 11, 2004, 12:55:28
Job time : 61 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:37 ; Search time 21 Seconds
(without alignments)
1717.706 Million cell updates/sec

Title: US-09-430-775-2
Perfect score: 1965
Sequence: 1 MNTSHLLALLLPKSPQGENR.....TVHTEVSKGSLRLSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1965	100.0	375	2	I39182	neuropeptide Y/pep
2	1962	99.8	375	2	G02300	pancreatic polypep
3	1519	77.3	375	2	S63685	neuropeptide Y rec
4	869	44.2	382	2	B46133	neuropeptide Y/pep
5	867	44.1	382	2	S27388	neuropeptide Y rec
6	856.5	43.6	384	2	A45490	neuropeptide Y/pep
7	823	41.9	366	2	S71152	neuropeptide Y/pep
8	822.5	41.9	349	2	S12863	G protein-coupled
9	483	24.6	370	1	I52315	G protein-coupled
10	468	23.8	381	2	I39187	neuropeptide Y/pep
11	430	21.9	423	2	B40470	glucocorticoid-ind
12	410	20.9	443	2	D40470	glucocorticoid-ind
13	395	20.1	455	2	T15622	hypothetical prote
14	387	19.7	491	2	C40470	glucocorticoid-ind
15	381.5	19.4	457	2	T29741	hypothetical prote
16	378.5	19.3	391	2	T32714	hypothetical prote
17	370.5	18.9	399	2	A46632	bombesin-like pept
18	368.5	18.8	394	2	JC7209	galanin receptor -
19	366	18.6	384	2	A39003	bombesin/gastrin-r
20	364	18.5	365	2	T20184	hypothetical prote
21	363	18.5	384	2	I57682	bombesin/ GRP rece
22	359	18.3	349	2	I59336	galanin receptor 1
23	358.5	18.2	399	2	S29480	bombesin receptor
24	357.5	18.2	384	2	A41007	gastrin-releasing
25	356	18.1	449	2	A41738	neuropeptide Y rec
26	345.5	17.6	376	2	I50102	Phe13 bombesin rec
27	339.5	17.3	412	2	T22076	hypothetical prote
28	337	17.2	357	2	JC7319	probable allatosta
29	337	17.2	423	2	JC7677	allatostatin recep
30	330.5	16.8	390	2	JH0374	bombesin receptor,
31	327	16.6	447	2	A47430	gastrin/cholecysto
32	326	16.6	444	2	A42685	cholecystokinin re
33	326	16.6	453	2	S32817	gastrin receptor -
34	326	16.6	584	2	JC7809	sulfakinin recepto
35	325.5	16.6	371	2	JC5796	probable chemoattr
36	325	16.5	427	2	S50150	gastric CCK-A rece
37	324.5	16.5	371	2	JC5498	G protein-coupled
38	323	16.4	440	2	A44081	kappa-type opioid
39	322	16.4	539	2	T27559	hypothetical prote
40	321.5	16.4	428	2	JN0692	cholecystokinin ty
41	321.5	16.4	436	2	JC5599	cholecystokinin-A
42	321	16.3	465	1	JQ1517	neurokinin 3 recep
43	320	16.3	385	2	S55524	neurokinin 3 recep
44	320	16.3	430	2	I51898	cholecystokinin A
45	320	16.3	452	2	A34916	neurokinin 3 recep

ALIGNMENTS

RESULT 1
I39182
neuropeptide Y/peptide YY receptor Y4 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000
C;Accession: I39182
R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.
J. Biol. Chem. 270, 26762-26765, 1995
A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic
A;Reference number: I39182; MUID:96070761; PMID:7592911
A;Accession: I39182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <RES>
A;Cross-references: EMBL:U35232; NID:g1063629; PIDN:AAC50280.1; PID:g1063630
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite

Query Match 100.0%; Score 1965; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.1e-161;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375
```

RESULT 2

```
G02300
pancreatic polypeptide receptor - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Apr-2000
C;Accession: G02300
R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01018
A;Accession: G02300
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-375 <YAN>
A;Cross-references: EMBL:U42387; NID:g1314327; PIDN:AAB07759.1; PID:g1314328
C;Superfamily: neurokinin 1 receptor

  Query Match             99.8%;  Score 1962;  DB 2;  Length 375;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-161;
  Matches  374;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTSVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375


RESULT 3
S63685
neuropeptide Y receptor D type - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
C;Accession: S63685
R;Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J.
FEBS Lett. 381, 58-62, 1996
A;Title: Cloning and characterization of a novel receptor to pancreatic polypeptide, a m
A;Reference number: S63685; MUID:96193913; PMID:8641440
A;Accession: S63685
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <GRE>
A;Cross-references: EMBL:U40189; NID:g1223969; PIDN:AAC52442.1; PID:g1223970
C;Superfamily: neurokinin 1 receptor

  Query Match             77.3%;  Score 1519;  DB 2;  Length 375;
  Best Local Similarity   75.9%;  Pred. No. 4.8e-123;
  Matches  283;  Conservative   35;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||| || | | | ||:| : || :|||||: |||| ::: ||:|:|||||::||||||
Db          1 MNTSHFLAPLFPGSLQGKNGTNPLDSPYNFSDGCQDSAELLAFIITTYSIETILGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:|||||||||||||||||||:||||| |||||||||||| |||| ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||||||||| |||||||:|| |:| |||||||| |
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSIFQAYLGIVVIWFISCFLSLPFLANSTL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ::|| |||| :||| ||||| || || |||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCIPLAFILVCYIRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| |||    | ||| ||::| :|: || |||||||||||||:|||: |||| |||
Db        241 LQRQKHVFHAHACSSRAGQMKRINSMLMTMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:|||||||||||||||||| ||||:|||||||   :|  ||||||||||||:
Db        301 NLIFLMCHLLAMASTCVNPFIYGFLNINFKKDIKALVLTCHCRSPQGESEHLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373


RESULT 4
B46133
neuropeptide Y/peptide YY receptor Y1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: B46133
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A;Title: Cloned human neuropeptide Y receptor couples to two different second messenger s
A;Reference number: A46133; MUID:92335184; PMID:1321422
A;Accession: B46133
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-382 <HER>
A;Note: sequence extracted from NCBI backbone (NCBIP:108539)
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

  Query Match             44.2%;  Score 869;  DB 2;  Length 382;
  Best Local Similarity   46.8%;  Pred. No. 4e-67;
  Matches  168;  Conservative   74;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:          |   : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db         16 YNVSENSPFLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | ||||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              ||||||||| ||:|:   ||:|| :|||:|   ||||:   || :   :| | |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:  :  |   |  |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::||:|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| ||  |||
Db        254 SSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::      |   :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 5
```

```
S27388
neuropeptide Y receptor NPY-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
C;Accession: S27388
R;Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.
FEBS Lett. 314, 285-288, 1992
A;Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex
A;Reference number: S27388; MUID:93106169; PMID:1468559
A;Accession: S27388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <EVA>
A;Cross-references: EMBL:Z18280; NID:g53438; PIDN:CAA79157.1; PID:g53439
C;Superfamily: neurokinin 1 receptor

  Query Match             44.1%;  Score 867;  DB 2;  Length 382;
  Best Local Similarity   46.5%;  Pred. No. 6e-67;
  Matches  167;  Conservative   75;  Mismatches  101;  Indels   16;  Gaps    4;

Qy          28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
               || ||:          |    : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db          16 YNASENSPLLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy          78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
               :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db          76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy         138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
               ||||||||| ||:|:   ||:|| :|||:|   ||||:   || :   :| |  |    |
Db         136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy         198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
               | || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:  :  |    |  |
Db         194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy         257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
               :   |::|::|: :|||||| |||| :||:: ||:|:  |  |: ||:||:||| || |||
Db         254 SSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy         317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
               |||  ||||| ||:::::   |   :  :: | : :||:||:||| ||:   :::|:
Db         314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 6
A45490
neuropeptide Y/peptide YY receptor Y1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: A45490; A46133; A42773
R;Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A;Title: Genomic organization, localization, and allelic differences in the gene for the
A;Reference number: A45490; MUID:93203272; PMID:8095935
A;Accession: A45490
A;Molecule type: DNA
A;Residues: 1-384 <HER>
A;Cross-references: GB:L07615; NID:g189284; PIDN:AAA59947.1; PID:g189285
A;Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBIP:128000)
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A;Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A;Reference number: A46133; MUID:92335184; PMID:1321422
A;Accession: A46133
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-384 <HE2>
A;Note: sequence extracted from NCBI backbone (NCBIP:108538)
R;Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.
J. Biol. Chem. 267, 10935-10938, 1992
A;Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
A;Reference number: A42773; MUID:92283782; PMID:1317848
A;Accession: A42773
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-384 <LAR>
A;Cross-references: GB:M88461; NID:g189155; PIDN:AAA73215.1; PID:g189156
A;Experimental source: fetal brain
A;Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBIP:104736)
C;Genetics:
A;Gene: GDB:NPY1R; NPYR
A;Cross-references: GDB:132643; OMIM:162641
A;Map position: 4q31.3-4q32
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester b
F;37-66/Domain: transmembrane #status predicted <TM1>
F;77-103/Domain: transmembrane #status predicted <TM2>
F;118-136/Domain: transmembrane #status predicted <TM3>
F;155-179/Domain: transmembrane #status predicted <TM4>
F;209-232/Domain: transmembrane #status predicted <TM5>
F;261-286/Domain: transmembrane #status predicted <TM6>
F;300-323/Domain: transmembrane #status predicted <TM7>
F;113-198/Disulfide bonds: #status predicted
F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;338/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             43.6%;  Score 856.5;  DB 2;  Length 384;
  Best Local Similarity   44.6%;  Pred. No. 4.8e-66;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy          16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
               | || |       ||||           |   : ::  :  :|    ::|| ||| |:
Db           8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy          65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
               : ::||| ||||:|| ||:||| |: ::| | | |||:||:|:||| :||:: |:||:|
Db          64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy         125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
               :|||| ||||:|:|||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db         124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy         185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
               :|    |:   || || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:
Db         184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy         245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
               :  |       |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db         242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy         304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
               ||:||| || ||||||  ||||| ||:::::      |   :  :: | : :||:||:|||
Db         302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy         364 GSLRLSGRSNPI 375
                 ||:   :::|:
Db         362 TSLK---QASPV 370


RESULT 7
S71152
neuropeptide Y/peptide YY receptor Y1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
C;Accession: S71152; S55924
R;Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.
submitted to the EMBL Data Library, November 1993
A;Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenop
A;Reference number: S71152
A;Accession: S71152
A;Molecule type: mRNA
A;Residues: 1-366 <MAR>
A;Cross-references: EMBL:L25416; NID:g409169; PIDN:AAA49918.1; PID:g409170
A;Experimental source: brain, hypothalumus
R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.
```

Biochim. Biophys. Acta 1261, 439-441, 1995
A;Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA f
A;Reference number: S55924; MUID:95260870; PMID:7742373
A;Accession: S55924
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-278,'T',280-366 <BLO>
A;Cross-references: EMBL:L25416; NID:g409169
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 41.9%; Score 823; DB 2; Length 366;
Best Local Similarity 44.4%; Pred. No. 3.5e-63;
Matches 161; Conservative 71; Mismatches 121; Indels 10; Gaps 4;

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Qy         18 ENRSKPLGTPYN----FSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKA 73
Db          8 ENLSVPNNISGNITFPISEDCALPLPMIFTLALAYGAVIILGLSGNLALIIIILKQKEMR 67

Qy         74 NVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLV 133
Db         68 NVTNILIVNLSFSDLLATIMCLPFTLIYTLMDHWIFGEVMCKLNEYIQCVSVTVSIFSLV 127

Qy        134 LVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALE 193
Db        128 LIAIERHQLIINPRGWRPNNRHACFGITVIWGFAMACSTPLMMYSVLTDEPFKNIS--LD 185

Qy        194 FLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHK-GT 252
Db        186 SYIGKYVCLEDFPEDKFRLSYTTLLFILQYLGPLCFIFVCYTKIFLRLKRRNNMMDKIRD 245

Qy        253 YSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAM 312
Db        246 NKYRSSETKRINIMLLSIVVGFALCWLPFFIFNLVFDWNHEAVATCNHNLLFLICHLTAM 305

Qy        313 ASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRS 372
Db        306 ISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSREDDYETIAMSTMHTDVSKTSLK---QA 362

Qy        373 NPI 375
Db        363 SPI 365
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RESULT 8
S12863
G protein-coupled receptor FC5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Apr-2000
C;Accession: S12863; S19101
R;Eva, C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
A;Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the
A;Reference number: S12863; MUID:91032093; PMID:2172008
A;Accession: S12863
A;Molecule type: mRNA
A;Residues: 1-349 <EVA>
A;Cross-references: EMBL:Z11504
R;Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
A;Description: Pharmacological and Transduction Properties of a Recombinantly Expressed
A;Reference number: S19101
A;Accession: S19101
A;Molecule type: mRNA
A;Residues: 1-343,'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNEKI' <KRA>
A;Cross-references: EMBL:Z11504; NID:g57636; PIDN:CAA77579.1; PID:g57637
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;39-61/Domain: transmembrane #status predicted <TM1>
F;73-93/Domain: transmembrane #status predicted <TM2>
F;114-135/Domain: transmembrane #status predicted <TM3>
F;155-175/Domain: transmembrane #status predicted <TM4>
F;213-231/Domain: transmembrane #status predicted <TM5>
F;262-285/Domain: transmembrane #status predicted <TM6>
F;299-322/Domain: transmembrane #status predicted <TM7>
F;2,11,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 41.9%; Score 822.5; DB 2; Length 349;
Best Local Similarity 48.5%; Pred. No. 3.6e-63;
Matches 157; Conservative 62; Mismatches 92; Indels 13; Gaps 3;

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Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
Db         16 YNVSENSPFLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
Db        254 SSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTC 340
Db        314 VNPIFYGFLNKNFQRDLQFFFNFC 337
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RESULT 9
I52315
G protein-coupled receptor UHR-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C;Accession: I52315
R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from r
A;Reference number: I52315; MUID:95251659; PMID:7733930
A;Accession: I52315
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-370 <RES>
A;Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528
C;Superfamily: neurokinin 1 receptor

Query Match 24.6%; Score 483; DB 1; Length 370;
Best Local Similarity 35.7%; Pred. No. 6.2e-34;
Matches 129; Conservative 59; Mismatches 129; Indels 44; Gaps 12;

```
Qy         11 LPKSPQGE----NRSKPLG-TPYNFS-EHCQDSVDVMV----------FI 44
Db          4 LPPGTTGDPDLFSGPSPAGSTPANQSAEASESNVSATVPRAAAVTPFQSLQLVHQLKGLI 63

Qy         45 VTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIM 104
Db         64 VMLYSIVVVVGLVGNCLLVLVIARVRRLHNVTNFLIGNLALSDVLMCAACVPLTLAYAFE 123

Qy        105 DY-WIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLI 163
Db        124 PRGWVFGGGLCHLVFFLQPVTVYVSVFTLTTIAVDRYVVLVHPLRRRISLKLSAYAVLGI 183

Qy        164 WVIACVLSLPFLANSILENVFHKNHSKALEFLADKVVCTESW-PLAHHRTIYTTFLLLFQ 222
Db        184 WALSAVLALPAAVHTY--HVELKPH--------DVRLCEEFWGSQERQRQIYAWGLLLGT 233

Qy        223 YCLPLGFILVCYARIYRRLQRQ---GRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWL 279
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Db        234 YLLPLLAILLSYVRVSVKLRNRVVPGSVTQSQADWDRA-RRRRTFCLLVVVVVVFALCWL 292

Qy        280 PLHVFNSLEDWHHEAI-PICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVL 338
              |||:|| | |     || |    | |: |:|| |||:| | ||||| :|: :|::|:: ::|
Db        293 PLHIFNLLRDLDPRAIDPYAFG-LVQLLCHWLAMSSACYNPFIYAWLHDSFREELRKMLL 351

Qy        339 T 339
              :
Db        352 S 352


RESULT 10
I39187
neuropeptide Y/peptide YY receptor Y2 - human
N;Alternate names: neuropeptide y/peptide YY receptor type 2
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000
C;Accession: I39187; I39163; G02301
R;Gerald, C.; Walker, M.W.; Vaysse, P.J.
J. Biol. Chem. 270, 26758-26761, 1995
A;Title: Expression cloning and pharmacological characterization of a human hippocampal
A;Reference number: I39187; MUID:96070760; PMID:7592910
A;Accession: I39187
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-381 <GER>
A;Cross-references: EMBL:U36269; NID:g1063633; PIDN:AAC50281.1; PID:g1063634
R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kie
J. Biol. Chem. 270, 22661-22664, 1995
A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptid
A;Reference number: I39163; MUID:96032678; PMID:7559383
A;Accession: I39163
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-133,'A',135-381 <ROS>
A;Cross-references: EMBL:U32500; NID:g1000750; PIDN:AAA93170.1; PID:g1000751
R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01019
A;Accession: G02301
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID:g1314330
C;Genetics:
A;Gene: GDB:NPY2R
A;Cross-references: GDB:4365607; OMIM:162642
A;Map position: 4q31-4q31
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F;49-76/Domain: transmembrane #status predicted <TM1>
F;87-113/Domain: transmembrane #status predicted <TM2>
F;166-186/Domain: transmembrane #status predicted <TM4>
F;221-237/Domain: transmembrane #status predicted <TM5>
F;269-291/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;123-203/Disulfide bonds: #status predicted
F;342/Binding site: palmitate (Cys) (covalent) #status predicted
F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             23.8%;  Score 468;  DB 2;  Length 381;
  Best Local Similarity   32.5%;  Pred. No. 1.2e-32;
  Matches  115;  Conservative   66;  Mismatches  127;  Indels   46;  Gaps    9;

Qy         38 VDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPL 97
              ::| | :: :|    ::||:|| :: | :: |    ||| |||| :| |: || |
Db         47 IEVQVVLILAYCSIILLGVIGNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPF 106

Qy         98 TAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAY 157
              |  ||:|  |  |  || :  : | ::| || ::| ::||:|: |:     | |   ::
Db        107 TLTYTLMGEWKMGPVLCHLVPYAQGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISF 166

Qy        158 LGIVLIWVIACVLSLP---FLANSILENVFHKNHSKALEFLADKVVCTESWP---LAHHR 211
              | | | | |: :|: |   |   |::| :         :|  : | ||| ||    : :
Db        167 LIIGLAWGISALLASPLAIFREYSLIEII--------PDF--EIVACTEKWPGEEKSIYG 216

Qy        212 TIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ------GRVFHKGTYSLRAGHMKQVNV 265
              |:|:   ||  | |||| |   | ||: :|:          :|:          ::
Db        217 TVYSLSSLLILYVLPLGIISFSYTRIWSKLKNHVSPGAANDHYHQ--------RRQKTTK 268

Qy        266 VLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFL 325
              :|| :|| ||| |||| |   |   : : :    ||| | |::|| ||  || :||::
Db        269 MLVCVVVVFAVSWLPLHAFQLAVDIDSQVLDLKEYKLIFTVFHIIAMCSTFANPLLYGWM 328

Qy        326 NTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVS-----KGSLRLSGRSNP 374
              |:|::|   :    |:|          |  :|:|||     | :| :   | |
Db        329 NSNYRKAFLS-AFRCEQR----------LDAIHSEVSVTFKAKKNLEVRKNSGP 371


RESULT 11
B40470
glucocorticoid-induced receptor precursor, short form RP23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C;Accession: B40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potenti
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: B40470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-423 <HAR>
A;Cross-references: GB:M80481; GB:M80610; NID:g193516; PIDN:AAA17882.1; PID:g460318
C;Superfamily: neurokinin 1 receptor

  Query Match             21.9%;  Score 430;  DB 2;  Length 423;
  Best Local Similarity   32.4%;  Pred. No. 2.6e-29;
  Matches  121;  Conservative   68;  Mismatches  142;  Indels   42;  Gaps   12;

Qy         17 GENRSKPLGTPYNFSEHCQDSV------------DVMVFIVTSYSIETVVGVLGNLCLMC 64
              | | |     | ||:  |: |             |   :: :||   |  : ||: :
Db         36 GPNASSHFWANYTFSD-WQNFVGRRRYGAESQNPTVKALLIVAYSFTIVFSLFGNVLVCH 94

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              |  : :   : |:| | ||| :| :: ||  | | |  :   |:||: :| :| | | |
Db         95 VIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTLVRFVNSTWVFGKGMCHVSRFAQYCS 154

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              : || |:|  :|:::|||:|::|   : ||::  : | :|||:|   |||   ::| : :|
Db        155 LHVSALTLTAIAVDRHQVIMHPLKPRISITKGVIYIAVIWVMATFFSLP---HAICQKLF 211

Qy        185 HKNHSKALEFLADKVVCTESWP----LAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
                 :|: :    : :|   :|    |          ||:||  | |||  | | |||: ::
Db        212 TFKYSEDIV----RSLCLPDFPEPADLFWKYLDLATFILL--YLLPLFIISVAYARVAKK 265

Qy        241 L---QRQGRVFHKGTYSLRAGHMKQVNV-VLVVMVVAFAVLWLPLHVFNSLEDWHHEAIP 296
              |       | |  :   :||     |:  | :||::|| ||: | ||: :  |       :
Db        266 LWLCNTIGDVTTEQYLALR--RKKKTTVKMLVLVVVLFALCWFPLNCYVLL----LSSKA 319

Qy        297 ICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLP--- 353
              |   | ::   |  ||:||| ||||| :|| ||: |:|||:  ||:  |  : : ||
Db        320 IHTNNALYFAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQR-PPKPQEDRLPSPV 378

Qy        354 --LSTVHTEVSKG 364
                 || | |
Db        379 PSFRVAWTEKSHG 391


RESULT 12
D40470
glucocorticoid-induced receptor, long form RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C;Accession: D40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
```

Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: D40470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-443 <HAR>
A;Cross-references: GB:M80160
C;Superfamily: neurokinin 1 receptor

Query Match 20.9%; Score 410; DB 2; Length 443;
Best Local Similarity 30.8%; Pred. No. 1.4e-27;
Matches 121; Conservative 68; Mismatches 142; Indels 62; Gaps 13;

```
Qy         17 GENRSKPLGTPYNFSEHCQDSV-----------DVMVFIVTSYSIETVVGVLGNLCLMC 64
Db         36 GPNASSHFWANYTFSD-WQNFVGRRRYGAESQNPTVKALLIVAYSFTIVFSLFGNVLVCH 94

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
Db         95 VIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTLVRFVNSTWVFGKGMCHVSRFAQYCS 154

Qy        125 VTVSILSLVLVALERHQ-------------------LIINPTGWKPSISQAYLGIVLIW 164
Db        155 LHVSALTLTAIAVDRHQRPWDFQESQSLHDTLFPPLEVIMHPLKPRISITKGVIYIAVIW 214

Qy        165 VIACVLSLPFLANSILENVFHKNHSKALEFLADKVVCTESWP----LAHHRTIYTTFLLL 220
Db        215 VMATFFSLP---HAICQKLFTFKYSEDIV----RSLCLPDFPEPADLFWKYLDLATFILL 267

Qy        221 FQYCLPLGFILVCYARIYRRL---QRQGRVFHKGTYSLRAGHMKQVNV-VLVVMVVAFAV 276
Db        268 --YLLPLFIISVAYARVAKKLWLCNTIGDVTTEQYLALR--RKKKTTVKMLVLVVVLFAL 323

Qy        277 LWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKAL 336
Db        324 CWFPLNCYVLL----LSSKAIHTNNALYFAFHWFAMSSTCYNPFIYCWLNENFRVELKAL 379

Qy        337 VLTCQQSAPLEESEHLP-----LSTVHTEVSKG 364
Db        380 LSMCQR-PPKPQEDRLPSPVPSFRVAWTEKSHG 411
```

RESULT 13
T15622
hypothetical protein C25G6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Apr-2000
C;Accession: T15622
R;Martin, J.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C25G6.
A;Reference number: Z18378
A;Accession: T15622
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-455 <MAR>
A;Cross-references: EMBL:U41028; NID:g1086712; PID:g1086716; PIDN:AAA82357.1; CESP:C25G6
C;Genetics:
A;Gene: CESP:C25G6.5
A;Introns: 37/3; 87/3; 137/2; 203/3; 260/2; 292/3; 346/2; 402/2
C;Superfamily: neurokinin 1 receptor

Query Match 20.1%; Score 395; DB 2; Length 455;
Best Local Similarity 30.8%; Pred. No. 2.9e-26;
Matches 102; Conservative 61; Mismatches 128; Indels 40; Gaps 11;

```
Qy         25 GTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLA 84
Db         30 GTEYSPKE-------FGYFITFAYMLIILFGAIGNFLTIIVVILNPAMRTTRNFFILNLA 82

Qy         85 FSDFLMCLLCQPLTAVYTIM-DYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLI 143
Db         83 LSDFFVCIVTAP-TTLYTVLYMFWPFSRTLCKIAGSLQGFNIFLSTFSIASIAVDRYVLI 141

Qy        144 INPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLADKV--VC 201
Db        142 IFPTKRERQQNLSFCFFIMIWVISLILAVPLLQASDLTPVF-------VEPSCDLALYIC 194

Qy        202 ---TESW-PLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRL------QRQGRVFHKG 251
Db        195 HEQNEIWEKMIISKGTYTLAVLITQYAFPLFSLVFAYSRIAHRMKLRFANRNQNVTTNTN 254

Qy        252 TYSLRAG---HMKQVNVVLVVMVVAFAVLWLPL---HVFNSLEDWHHEAIPICHGNLIFL 305
Db        255 TSQRRRSVVERQRRTHLLLVCVVAVFAVAWLPLNVFHIFNTFELVNSFSV------TTFS 308

Qy        306 VCHLLAMASTCVNPFIYGFLNTNFKKEIKAL 336
Db        309 ICHCLAMCSACLNPLIYAFFNHNFRIEFMHL 339
```

RESULT 14
C40470
glucocorticoid-induced receptor, long form RP82 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C;Accession: C40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potenti
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: C40470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-491 <HAR>
A;Cross-references: GB:M80610
C;Superfamily: neurokinin 1 receptor

Query Match 19.7%; Score 387; DB 2; Length 491;
Best Local Similarity 28.1%; Pred. No. 1.5e-25;
Matches 124; Conservative 66; Mismatches 141; Indels 110; Gaps 16;

```
Qy         17 GENRSKPLGTPYNFSEHCQDSV-----------DVMVFIVTSYSIETVVGVLGNLCLMC 64
Db         36 GPNASSHFWANYTFSD-WQNFVGRRRYGAESQNPTVKALLIVAYSFTIVFSLFGNVLVCH 94

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
Db         95 VIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTLVRFVNSTWVFGKGMCHVSRFAQYCS 154

Qy        125 VTVSILSLVLVALERH----------------QLIINPTG-------------------- 148
Db        155 LHVSALTLTAIAVDRHQGLTAIAVDRHQGLELQKMVRPRGDGGELRSPSVTFVPSSLCPA 214

Qy        149 -------W-----------------------KP--SISQAYLGIVLIWVIACVLSLPFLA 176
Db        215 LFTCKRPWDFQESQSLHDTLFPPLEVIMHPLKPRISITKGVIYIAVIWVMATFFSLP--- 271

Qy        177 NSILENVFHKNHSKALEFLADKVVCTESWP----LAHHRTIYTTFLLLFQYCLPLGFILV 232
Db        272 HAICQKLFTFKYSEDIV----RSLCLPDFPEPADLFWKYLDLATFILL--YLLPLFIISV 325

Qy        233 CYARIYRRL---QRQGRVFHKGTYSLRAGHMKQVNV-VLVVMVVAFAVLWLPLHVFNSLE 288
Db        326 AYARVAKKLWLCNTIGDVTTEQYLALR--RKKKTTVKMLVLVVVLFALCWFPLNCYVLL- 382

Qy        289 DWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEE 348
Db        383 ---LSSKAIHTNNALYFAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQR-PPKPQ 438

Qy        349 SEHLP-----LSTVHTEVSKG 364
Db        439 EDRLPSPVPSFRVAWTEKSHG 459
```

RESULT 15
T29741
hypothetical protein C39E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Apr-2000
C;Accession: T29741
R;Fulton, B.; Le, T.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C39E6.
A;Reference number: Z20676
A;Accession: T29741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-457 <FUL>
A;Cross-references: EMBL:U49944; PIDN:AAA93419.1; CESP:C39E6.6
C;Genetics:
A;Gene: CESP:C39E6.6
A;Introns: 58/3; 107/1; 169/3; 253/3; 274/2; 329/2; 366/2; 438/2
C;Superfamily: neurokinin 1 receptor

Query Match 19.4%; Score 381.5; DB 2; Length 457;
Best Local Similarity 25.9%; Pred. No. 4.2e-25;
Matches 104; Conservative 81; Mismatches 143; Indels 73; Gaps 10;

```
Qy         29 NFSEHCQ----------DSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNL 78
              ||:: ||            |:  :|  :| |      :|: ||: |: ||   |   :| |:
Db          5 NFTD-CQVYWKVYPDPSQSIYAIVPFLTVYLFLFFLGLFGNVTLIYVTCSHKALLSVQNI 63

Qy         79 LIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALE 138
               | ||| || :||:|  |:| :  :   | ||  || :   || :|: |   ||  :||:
Db         64 FILNLAASDCMMCILSLPITPITNVYKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALD 123

Qy        139 RHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLADK 198
              |: |:: |     |   |:|  ||:|::: |::||:  |           : :|:  ::
Db        124 RYILVVRPHSTPLSQRGAFLTTVLLWILSFVVTLPYAFN----------MQMIEYTEER 172

Qy        199 V---VCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIY----RRLQRQGRVFHKG 251
              :    ||| |  |  |  ||  ::| |: :|   :  ||| |     :| | : |   :
Db        173 ICGYFCTEKWESAKSRRAYTMIVMLAQFVVPFAVMAFCYANIVSVLSKRAQTKIRKMVER 232

Qy        252 TYSLRAG-------------------------------HMKQVNVVLVVMVVAFAVLWLP 280
              | :| :                              ::   :|| ||| | : |||
Db        233 TSALESSCAFPSHGLEQYENELNEFLDKQEKEKQRVVLQNRRTTSILVTMVVWFGITWLP 292

Qy        281 LHVFNSLEDWHH-EAIPICHGN-------LIFLVCHLLAMASTCVNPFIYGFLNTNFKKE 332
               :| : : ::   ::    :|         |: |  | :||::  :|| :| :|| :|::
Db        293 HNVISLIIEYDDTQSFFRLYGRDDYDISYLLNLFTHSIAMSNNVLNPVLYAWLNPSFRQ- 351

Qy        333 IKALVLTCQQSAPLEESEHLPLSTVH-TEVSKGSLRLSGRS 372
              ||:         :    :  ::|: |::   :  |:||:
Db        352 ---LVIKTYFGDRRKSDRIINQTSVYKTKIVHDTKHLNGRA 389
```

Search completed: May 11, 2004, 12:57:28
Job time : 23 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:37 ; Search time 45 Seconds
(without alignments)
2629.318 Million cell updates/sec

Title: US-09-430-775-2
Perfect score: 1965
Sequence: 1 MNTSHLLALLLPKSPQGENR.....TVHTEVSKGSLRLSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1756	89.4	375	6	O97505	O97505 sus scrofa
2	1633.5	83.1	372	11	Q9Z2D4	Q9z2d4 cavia porce
3	1517	77.2	375	11	Q8BZF9	Q8bzf9 mus musculu
4	1192.5	60.7	377	13	Q8QGM3	Q8qgm3 gallus gall
5	960	48.9	375	13	O57463	O57463 brachydanio
6	950.5	48.4	373	13	O73734	O73734 brachydanio
7	922	46.9	374	13	Q9YHX1	Q9yhx1 gadus morhu
8	915.5	46.6	377	13	O73733	O73733 brachydanio
9	890.5	45.3	365	13	Q8UVW7	Q8uvw7 lampetra fl
10	859.5	43.7	385	13	Q8QFM1	Q8qfm1 gallus gall
11	856.5	43.6	383	6	Q9GK75	Q9gk75 macaca mula
12	573	29.2	290	4	Q99463	Q99463 homo sapien
13	487	24.8	443	13	Q8QFM2	Q8qfm2 gallus gall
14	471	24.0	381	11	Q8BWV1	Q8bwv1 mus musculu
15	469	23.9	381	11	Q9ERC0	Q9erc0 rattus norv
16	467.5	23.8	446	11	Q925F1	Q925f1 cavia porce
17	467	23.8	600	5	Q9VW75	Q9vw75 drosophila
18	465.5	23.7	445	6	Q9GK73	Q9gk73 macaca mula
19	457.5	23.3	481	5	Q9VNM1	Q9vnm1 drosophila
20	457.5	23.3	485	5	Q8SZ35	Q8sz35 drosophila
21	422.5	21.5	422	11	Q8VHD7	Q8vhd7 rattus norv
22	415	21.1	365	11	Q8BHH0	Q8bhh0 mus musculu
23	403.5	20.5	405	11	Q924N0	Q924n0 mus musculu
24	403	20.5	432	11	Q924G9	Q924g9 rattus norv
25	397	20.2	456	11	Q80T54	Q80t54 mus musculu
26	395	20.1	417	11	Q8BKR6	Q8bkr6 mus musculu
27	394	20.1	417	11	Q924H0	Q924h0 mus musculu
28	393.5	20.0	465	5	O44426	O44426 lymnaea sta
29	392.5	20.0	463	11	Q9EPJ7	Q9epj7 mus musculu
30	381.5	19.4	457	5	Q18534	Q18534 caenorhabdi
31	378.5	19.3	391	5	Q9GZG8	Q9gzg8 caenorhabdi
32	374	19.0	387	5	Q22188	Q22188 caenorhabdi
33	374	19.0	402	5	Q964E5	Q964e5 dugesia tig
34	374	19.0	430	5	Q8I0L4	Q8i0l4 caenorhabdi
35	372	18.9	336	5	Q9Y073	Q9y073 lymnaea sta
36	372	18.9	402	5	Q20275	Q20275 caenorhabdi
37	368.5	18.8	394	5	Q9U721	Q9u721 drosophila
38	368.5	18.8	540	5	Q9VRM0	Q9vrm0 drosophila
39	366	18.6	380	5	Q9NFV0	Q9nfv0 lymnaea sta
40	364	18.5	365	5	Q9XXU4	Q9xxu4 caenorhabdi
41	363	18.5	384	11	Q9QW13	Q9qw13 rattus sp.
42	363	18.5	517	5	Q9VWR3	Q9vwr3 drosophila
43	360	18.3	425	4	Q9HBV6	Q9hbv6 homo sapien
44	359.5	18.3	399	11	Q8K418	Q8k418 rattus norv
45	358	18.2	380	5	Q9NFV3	Q9nfv3 lymnaea sta

ALIGNMENTS

RESULT 1
O97505
ID O97505 PRELIMINARY; PRT; 375 AA.
AC O97505;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y receptor type 4 (Neuropeptide Y-family receptor
DE Y4).
GN NPY Y4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LWD; TISSUE=Kidney;
RA Ito Y., Minezawa M.;
RT "Sus scrofa NPY Y4 gene for neuropeptide Y receptor type 4, complete
RT cds [genomic].";
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED NORWEGIAN LANDRACE;
RX MEDLINE=20187975; PubMed=10720571;
RA Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P.,
RA Andersson L., Lundin L.-G., Larhammar D.;
RT "Evolution of the neuropeptide Y receptor family: gene and chromosome
RT duplications deduced from the cloning and mapping of the five receptor
RT subtype genes in the pig.";
RL Genome Res. 10:302-310(2000).
DR EMBL; AB021678; BAA36218.1; -.
DR EMBL; AF227955; AAF62507.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

```
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Neuropeptide; Receptor.
SQ   SEQUENCE   375 AA;  42346 MW;  5992F075904DB1A0 CRC64;

  Query Match             89.4%;  Score 1756;  DB 6;  Length 375;
  Best Local Similarity   85.9%;  Pred. No. 9.1e-157;
  Matches  322;  Conservative   29;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||  ||  |  ||  | :|||:||||  |  |||||:|||||:|  |||:||||||||:|||||||
Db          1 MNISHFLGLLLFPGAPQGQNRSKAKGIPYNFSDHCQDSIDPMVFVVTSYSIETIVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||:|||:|||||||||||||||||||||||:||||||:|||||||:||| |||:||||
Db         61 CLICVTIRQKEKANVTNLLIANLAFSDFLMCLICQPLTAIYTIMDYWVFGEVLCKISAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||:||||||||:||:||| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSVSQAYLGIVVIWLIACFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              :||||||||||:|||||||||||||| ||| ||||||||||||:|| ||||||  |||:|
Db        181 QNVFHKNHSKAVEFLADKVVCTESWPLEHHRIIYTTFLLLFQYCIPLAFILVCYVRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |:::|||||||  ||  ||  ||::| :|  ||||||||||||||||||:|||||||||
Db        241 LRKRGRVFHKGAYSSRAWQMKRINGILAAMVVAFAVLWLPLHVFNSLEDWYHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||:|||||||||  |:||||||||||  ||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEVKALVLTCQQSIPVEESEHLPLSTVQTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              :|||||||||||||
Db        361 ISKGSLRLSGRSNPI 375


RESULT 2
Q9Z2D4
ID   Q9Z2D4      PRELIMINARY;      PRT;   372 AA.
AC   Q9Z2D4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Pancreatic polypeptide receptor Y4.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99017377; PubMed=9802391;
RA   Eriksson H., Berglund M.M., Holmberg S.K., Kahl U., Gehlert D.R.,
RA   Larhammar D.;
RT   "The cloned guinea pig pancreatic polypeptide receptor Y4 resembles
RT   more the human Y4 than does the rat Y4.";
RL   Regul. Pept. 75:29-37(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sharma P.S., Holmberg S.K., Eriksson H., Beck-Sickinger A.G.,
RA   Grundemar L., Larhammar D.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF072822; AAD13144.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   372 AA;  41774 MW;  5B6CF78FBB213374 CRC64;

  Query Match             83.1%;  Score 1633.5;  DB 11;  Length 372;
  Best Local Similarity   82.9%;  Pred. No. 3e-145;
  Matches  311;  Conservative   22;  Mismatches   39;  Indels    3;  Gaps    1;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              |:||  ||  |||  ||  ||  |||     :|||:||||| |:|  ||||||  |||:|||||||
Db          1 MDTSPFLASLLPTYPQEENSSKPQRLLFNFSDHCQDSGDLMGFIVTSYGIETIVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||:|:|:|||||||||:|||||||||||||||:|||||  :|||||||||||  ||||||||
Db         61 CLICMTLRQKEKANVTSLLIANLAFSDFLMCLICQPLTVIYTIMDYWIFGEVLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||: |||||||:||:|||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSVPQAYLGIVVIWLIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              |||||||||||  || ||| | |||||  ||| :|||||||||||:|| ||||||  ||  |
Db        181 ENVFHKNHSKALAFLEDKVACKESWPLGHHRVVYTTFLLLFQYCIPLAFILVCYLRISWR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |:|||||  |  | |||  ||::|  |||  ||  |||||||||||||||||||||:|||
Db        241 LRRQGRVLCK---SSRAGQMKRINGVLVAMVGAFAVLWLPLHVFNSLEDWHHEAIPVCHG 297

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||:||||||||| |  |||||||:|||
Db        298 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEVKALVLTCQQSLPPEESEHLPLSTLHTE 357

Qy        361 VSKGSLRLSGRSNPI 375
              ||||  |  |  ||||||
Db        358 VSKGFLPLGGRSNPI 372


RESULT 3
Q8BZF9
ID   Q8BZF9      PRELIMINARY;      PRT;   375 AA.
AC   Q8BZF9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neuropeptide Y receptor type 4.
GN   PPYR1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK035505; BAC29082.1; -.
DR   MGD; MGI:105374; Ppyr1.
DR   GO; GO:0001602; F:pancreatic polypeptide receptor activity; IDA.
DR   GO; GO:0001601; F:peptide YY receptor activity; IDA.
DR   InterPro; IPR000362; Fumarate_lyase.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00163; FUMARATE_LYASES; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ   SEQUENCE   375 AA;  42657 MW;  638EBA110E7F7A53 CRC64;

  Query Match             77.2%;  Score 1517;  DB 11;  Length 375;
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  Best Local Similarity   75.6%;  Pred. No. 2.7e-134;
  Matches  282;  Conservative   35;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||| || | | | ||:| : || :|||||: |||| ::: ||:|:|||||::||||||
Db          1 MNTSHFLAPLFPGSLQGKNGTNPLDSPYNFSDGCQDSAELLAFIITTYSIETILGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:||||||||||||||||||:|||||  ||||||||||| |||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||| |||||||:| ::| |||||||| |
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSIFQAYLGIVVIWFVSCFLSLPFLANSTL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| ||||| ||   ||| ||||||||||||:|| |||||| ||| |
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCIPLAFILVCYIRIYHR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| |||     | ||| ||::| :|: || |||||||||||||:||||: |||| |||
Db        241 LQRQKHVFHAHACSSRAGQMKRINSMLMTMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNPKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:||||||||||||||||| ||||:|||||||   :|  ||||||||||||:
Db        301 NLIFLMCHLLAMASTCVNPFIYGFLNINFKKDIKALVLTCHCRSPRGESEHLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373


RESULT 4
Q8QGM3
ID   Q8QGM3      PRELIMINARY;      PRT;   377 AA.
AC   Q8QGM3;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y receptor 4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lundell I., Boswell T., Larhammar D.;
RT   "Chicken Neuropeptide Y Family Receptor Y4; a Receptor with Equal
RT   Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF410853; AAL84161.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   377 AA;  42972 MW;  C9EC6C00DBFD1F9E CRC64;

  Query Match             60.7%;  Score 1192.5;  DB 13;  Length 377;
  Best Local Similarity   60.4%;  Pred. No. 8.9e-104;
  Matches  218;  Conservative   60;  Mismatches   80;  Indels    3;  Gaps    1;

Qy         18 ENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              :| |      | : |   |::   |: ||: ||||:|||:|::||:||: |  ||||| ||||
Db         17 KNLSSNRSFPSHLSNQCRNVTDLTVFLATSYSLETVLGIVGNICLIAVIARQKEKTNVTN 76

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :||:||  ||  |||:| | | |||:|||||||| :|||::| || ||||||||||||:||
Db         77 ILISNLIISDLFMCLVCLPFTVVYTMMDYWIFGEVMCKMTSFTQCTSVTVSILSLVLIAL 136

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              |||||||||||:|||||||||| :|| :||::|||||  ||| |  ::  |  : |  |
Db        137 ERHQLIINPTGWRPSISQAYLGIGVIWTLACLMSLPFLTTSILSNDLYEQLSHIMNFSYD 196

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYSLRA 257
              | :| :|||   || |||| ||| |||:|| ||::|| ||| |||::  :| |  || ||
Db        197 KAICIDSWPSEQHRLIYTTTLLLLQYCIPLFFIILCYLRIYLRLQKRKDMFEKSEYSNRA 256

Qy        258 GHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCV 317
              ::::|::|  || |||| ||||||||:: ||::: |  || |||| :|||:|||||||
Db        257 VQLRRINILLASMVAAFAVCWLPLHVFNTIVDWNYKIISPCHHNLIFSLCHLVAMASTCV 316

Qy        318 NPFIYGFLNTNFKKEIKALVLTCQQ---SAPLEESEHLPLSTVHTEVSKGSLRLSGRSNP 374
              || ||||||:|||||:|:|:|:||    :| :|: :|||||: |||||||| |: | |
Db        317 NPVIYGFLNSNFKKEVKSLILSCQHNSVTASIEDYDHLPLSTMQTEVSKGSLSLNCRHNS 376

Qy        375 I 375
              |
Db        377 I 377


RESULT 5
O57463
ID   O57463      PRELIMINARY;      PRT;   375 AA.
AC   O57463;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y /peptide YY receptor Yb.
GN   NPYRYB.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lundell I., Berglund M.M., Starback P., Salaneck S., Gehlert D.R.,
RA   Larhammar D.;
RT   "Cloning and characterization of a novel neuropeptide Y (NPY) receptor
RT   subtype in the zebrafish.";
RL   DNA Cell Biol. 0:0-0(1997).
DR   EMBL; AF030245; AAB94616.1; -.
DR   ZFIN; ZDB-GENE-980526-208; npyryb.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   375 AA;  42116 MW;  4B0C9551131A14D1 CRC64;

  Query Match             48.9%;  Score 960;  DB 13;  Length 375;
  Best Local Similarity   50.1%;  Pred. No. 6.5e-82;
  Matches  188;  Conservative   57;  Mismatches  112;  Indels   18;  Gaps    3;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              |  |||          | |  |  |      |  |:    |:: :||    ||::||
Db          1 MERSHL----------NNSSWLLEDP-----TCPASLSSTTFLIVAYSTMLAVGLVGNT 44

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: |  |||| ||||: | ||: || |:||:| |:| :||:|| || || |||:: |:
Db         45 CLVVVITRQKEMRNVTNIFIVNLSCSDILVCLVCLPVTIIYTLMDRWILGEALCKVTPFV 104

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||| |:||:||||||||||:|||||| :  :|| : :||:||| :|||||: :||
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Db        105 QCMSVTVSIFSMVLIALERHQLIIHPTGWKPVVRHSYLAVAVIWIIACFISLPFLSFNIL 164

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Db        165 TNSPFHNLSLPFNPFSDHFICIEQWPSEGNRLTYTTTLLLCQYCLPLALILVCYFRIFLR 224

Qy        241 LQRQGRVFH--KGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPIC 298

Db        225 LSRRKDMVERARGGRQKKAKGSKRVNAMLASIVAAFALCWLPLNVFNTIFDWNHEAIPVC 284

Qy        299 HGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVH 358

Db        285 QHDAIFSACHLTAMASTCVNPVIYGFLNNNFQKELKSLLSRCRCWGPAESYESFPLSTVS 344

Qy        359 TEVSKGSLRLSGRSN 373

Db        345 TGITKGSILSNGSAS 359


RESULT 6
O73734
ID   O73734      PRELIMINARY;      PRT;   373 AA.
AC   O73734;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y/peptide YY receptor Yc.
GN   NPYRYC OR NPYRYC.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98068842; PubMed=9407007;
RA   Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
RA   Larhammar D.;
RT   "Cloning and characterization of a novel neuropeptide Y receptor
RT   subtype in the zebrafish.";
RL   DNA Cell Biol. 16:1357-1363(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98096393; PubMed=9434780;
RA   Ringvall M., Berglund M.M., Larhammar D.;
RT   "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
RT   subtype in the zebrafish.";
RL   Biochem. Biophys. Res. Commun. 241:749-755(1997).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF037401; AAC41277.1; -.
DR   ZFIN; ZDB-GENE-990415-175; npyryc.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   373 AA;  41673 MW;  217DA7F51A940CFD CRC64;

  Query Match             48.4%;  Score 950.5;  DB 13;  Length 373;
  Best Local Similarity   53.6%;  Pred. No. 5e-81;
  Matches  181;  Conservative   60;  Mismatches   94;  Indels    3;  Gaps    2;

Qy         31 SEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLM 90

Db         20 SNVCPPSVSGTTLLIVAYSTVIAVGLVGNTCLVFIISRQKEMRNVTNILIANLSCSDILM 79

Qy         91 CLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWK 150

Db        105 QCMSVTVSIFSMVLIALERHQLIIHPTGWKPVVRHSYLAVAVIWIIACFISLPFLSFNIL 164

Qy        151 PSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLADKVVCTESWPLAHH 210

Db        140 PAAGHSYLAVAVTWMVACFISLPFLSFNILTNAPFQNISLPFNPFSDHVICMELWPSERN 199

Qy        211 RTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS--LRAGHMKQVNVVLV 268

Db        200 RLAYTTSLLLFQYCLPLLLLILLCYLRIFLRLRRRKDMVEQATEARQRKARGAQRVNAMLV 259

Qy        269 VMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTN 328

Db        260 VIVVAFALCWLPLNVFNTIFDWYHQALPACQHDVIFSACHLTAMASTCVNPVVYGFLNTN 319

Qy        329 FKKEIKALVLTCQQSAPLEES-EHLPLSTVHTEVSKGS 365

Db        320 FQKELKATLQRCNCGWGVPETYESFPLSTVATDVSKVS 357


RESULT 7
Q9YHX1
ID   Q9YHX1      PRELIMINARY;      PRT;   374 AA.
AC   Q9YHX1;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y/peptide YY receptor Yb.
GN   NPYRB.
OS   Gadus morhua (Atlantic cod).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX   NCBI_TaxID=8049;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99017378; PubMed=9802392;
RA   Arvidsson A.K., Wraith A., Jonsson-Rylander A.C., Larhammar D.;
RT   "Cloning of a neuropeptide Y/peptide YY receptor from the Atlantic
RT   cod: the Yb receptor.";
RL   Regul. Pept. 75:39-43(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF073925; AAD02833.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   374 AA;  42260 MW;  D2A9C9516C4998E2 CRC64;

  Query Match             46.9%;  Score 922;  DB 13;  Length 374;
  Best Local Similarity   51.3%;  Pred. No. 2.4e-78;
  Matches  178;  Conservative   62;  Mismatches   95;  Indels   12;  Gaps    4;

Qy         32 EHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMC 91

Db         28 EECPSSKSGTTFLILVYSTMIAVGIVGNSCLVFVIARQKEMHNVTNIFIANLSCSDILMC 87

Qy         92 LLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKP 151

Db         88 IFCLPVTLIYTLMDRWILGEALCKLTPFVQCISVTVSIFSLVLIAMERYQLIIHPTGWKP 147

Qy        152 SISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLA-DKVVCTESWPLAHH 210

Db        148 MVGQSYMAVGIIWVVACLISVPFLSFTVLDNLPLQNLS--LPFPGQDHWLCTESWPTNSN 205

Qy        211 RTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYSLRAGHMK---QVNVVL 267
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Db        206 RLAYTTSLLVFQYFLPLGLIAACYLSIFLRLRRRKDMVERARDSSRDNRAKGSRRINVML 265

Qy        268 VVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNT 327

Db        266 GSIVALFAVCWLPLNIFNTVFDWHHELMVSCQHNLIFSVCHLVAMASTCVNPVVYGFLNS 325

Qy        328 NFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEV------SKGSLRL 368

Db        326 NFQKQLKATLSHCRCWGAAERYENLPLSAVSTEVTKESHMSKGSISI 372


RESULT 8
O73733
ID   O73733      PRELIMINARY;      PRT;   377 AA.
AC   O73733;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y/peptide YY receptor Ya.
GN   NPYRYA OR NPYRYA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98068842; PubMed=9407007;
RA   Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
RA   Larhammar D.;
RT   "Cloning and characterization of a novel neuropeptide Y receptor
RT   subtype in the zebrafish.";
RL   DNA Cell Biol. 16:1357-1363(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98096393; PubMed=9434780;
RA   Ringvall M., Berglund M.M., Larhammar D.;
RT   "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
RT   subtype in the zebrafish.";
RL   Biochem. Biophys. Res. Commun. 241:749-755(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99337783;
RA   Starback P., Lundell I., Fredriksson R., Berglund M.M., Yan Y.L.,
RA   Wraith A., Soderberg C., Postlethwait J.H., Larhammar D.;
RT   "Neuropeptide Y receptor subtype with unique properties cloned in the
RT   zebrafish: the zYa receptor.";
RL   Brain Res. Mol. Brain Res. 70:242-252(1999).
DR   EMBL; AF037400; AAC41276.1; -.
DR   HSSP; P02699; 1F88.
DR   ZFIN; ZDB-GENE-980526-393; npyrya.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   377 AA;  42901 MW;  60E62AD9C7BFB5D0 CRC64;

  Query Match           46.6%;  Score 915.5;  DB 13;  Length 377;
  Best Local Similarity   49.1%;  Pred. No. 1e-77;
  Matches  172;  Conservative   70;  Mismatches   89;  Indels   19;  Gaps    5;

Qy         34 CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLL 93

Db         35 CWQSSTMTLTLVLCYCLVLILGLLGNILLICIIMHQRDPPNVTSILIANLSVSDILVSVF 94

Qy         94 CQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSI 153

Db         95 CLPFTVVYTLMDHWIFGALLCRLMPFVQCVSVTVSVLSLVLIALERHQLILHPSGWKPSV 154

Qy        154 SQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEF----LADKVVCTESWPLAH 209

Db        155 PQAYIAVLTVWLLACVTSLPFLA-------FHLLTSEPYSLFPAPLSQLQVCLEVWPSQD 207

Qy        210 HRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVF------HKGTYSLRAGHMKQV 263

Db        208 HKLAYTTSLLLFQYCCPLLLMLLCYLRIFLRLQRRERMLERQCSRNREDEHRRVMHSKRI 267

Qy        264 NVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYG 323

Db        268 NVMLATLVAAFAVCWLPLNAFNVVADCDQEVLPVCNHNLLFSLCHLLAMSSTCVNPIIYG 327

Qy        324 FLNTNFKKEIKALVLTCQQSAPLEES-EHLPLSTVHTEVSKGSLRLSGRS 372

Db        328 FLNSNFRKDVASVVLHC-HFQPLEDSYEHFPMSTMNTDVSRTSFRLRNNS 376


RESULT 9
Q8UVW7
ID   Q8UVW7      PRELIMINARY;      PRT;   365 AA.
AC   Q8UVW7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   NPY receptor.
OS   Lampetra fluviatilis (River lamprey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC   Petromyzontiformes; Petromyzontidae; Lampetra.
OX   NCBI_TaxID=7748;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21590343; PubMed=11733009;
RA   Salaneck E., Fredriksson R., Larson E.T., Conlon J.M., Larhammar D.;
RT   "A neuropeptide Y receptor Y1-subfamily gene from an agnathan, the
RT   European river lamprey. A potential ancestral gene.";
RL   Eur. J. Biochem. 268:6146-6154(2001).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF340022; AAL66410.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   365 AA;  41060 MW;  9EE5FD3BBE6807E9 CRC64;

  Query Match           45.3%;  Score 890.5;  DB 13;  Length 365;
  Best Local Similarity   48.3%;  Pred. No. 2.2e-75;
  Matches  172;  Conservative   67;  Mismatches  106;  Indels   11;  Gaps    2;

Qy         29 NFSE-------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIA 81

Db          8 NWSEMPQLDLDHCQTPQAVRSFVIATYCVLIALGLLGNSLLVLVILRHSELHNVTNILIV 67

Qy         82 NLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQ 141

Db         68 NLAFSDMLVGLVCLPLTIAYTLMDHWIFGEALCKGSPFLQCSAVSVSIFSLVLIAIERHQ 127

Qy        142 LIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLADKVVC 201

Db        128 LIINPTGWKPSLNHAYVAIGAIWVAAFAMSSPFLAFHVLTDEPYRNLSHYFPDYGEKVAC 187

Qy        202 TESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVF----HKGTYSLRA 257

Db        188 IEVVALGHLKFAFTTSLLVFQFSCPLLFVFLCYLRIFLRLRQRKKMLPTGREGGGNGVRA 247
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Qy        258 GHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCV 317
              |||::|::|| :|  ||: |||| ||:: ||:   :  |  :||| :||| || | |:
Db        248 SHMKKINMMLVAIVAGFAICWLPLYTFNAVSDWNPTLLLHCQHDLIFSLCHLTAMLSICI 307

Qy        318 NPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSN 373
              ||  ||||| || ||:|| :| ||  :   |: |: ||||::|::|||||| | :::
Db        308 NPIFYGFLNNNFLKELKATILRCQCNPVEEDFENYPLSTMNTDISKGSLRFSCKNS 363


RESULT 10
Q8QFM1
ID   Q8QFM1      PRELIMINARY;      PRT;   385 AA.
AC   Q8QFM1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y receptor Y1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22060921; PubMed=12065655;
RA   Holmberg S.K.S., Mikko S., Boswell T., Zoorob R., Larhammar D.;
RT   "Pharmacological characterization of cloned chicken neuropeptide Y
RT   receptors Y1 and Y5.";
RL   J. Neurochem. 81:462-471(2002).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AY040845; AAK83557.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   385 AA;  44365 MW;  DBAA905C89D3AE84 CRC64;

  Query Match           43.7%;  Score 859.5;  DB 13;  Length 385;
  Best Local Similarity   44.5%;  Pred. No. 1.9e-72;
  Matches  173;  Conservative   74;  Mismatches  111;  Indels   31;  Gaps    7;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFS----------EHCQDSVDVMVFIVTSYS 49
              || | |        | | | |        |||           | |   : ::  :  :|
Db          1 MNASVL-------DPLGNNSSH-----LNFSEKNSQILQFEDEDCHVPLAMVFTLALAYG 48

Qy         50 IETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIF 109
                ::|| ||| |: : ::|||  ||||:|| ||:||| |: ::| | | |||:|||:|||
Db         49 TVIILGVSGNLALIVIILKQKEMRNVTNILIVNLSFSDLLVTIMCLPFTFVYTLMDHWIF 108

Qy        110 GETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACV 169
              || :||:: |:|| |:||: ||||:|:||||||||| ||:|:   ||:|| |||:|
Db        109 GEAMCKLNPFVQCASITVSVFSLVLIAIERHQLIINPRGWRPNNRHAYMGIAAIWVLATA 168

Qy        170 LSLPFLANSILENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGF 229
              |||||   :| :   :| :   :   || || : :||   |  ||| ||: ||  || |
Db        169 SSLPFLIYHVLTDEPFRNIT--FDEYKDKYVCLDLFPLDTARLSYTTTLLVIQYFGPLCF 226

Qy        230 ILVCYARIYRRLQRQGRVFHKGTYS-LRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLE 288
              | :|| :|| ||:::  :  |   |  |:   |::|::|: :|||||| |||| :|| :
Db        227 IFICYLKIYFRLKKRSNMMDKMRDSKYRSSETKRINIMLISIVVAFAVCWLPLTIFNIVF 286

Qy        289 DWHHEAIPI--CHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPL 346
              ||:|| :|:  |  ||:||:||| || ||||||  ||||| ||:::: |   |   :
Db        287 DWNHEILPVATCSHNLLFLICHLTAMISTCVNPIFYGFLNKNFQRDLQFLFHFCHFRSRE 346

Qy        347 EESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |: | : :||:||:||| ||:   :::|:
Db        347 EDYETIAMSTMHTDVSKTSLK---QASPV 372


RESULT 11
Q9GK75
ID   Q9GK75      PRELIMINARY;      PRT;   383 AA.
AC   Q9GK75;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y receptor Y1.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21184974; PubMed=11287088;
RA   Gehlert D.R., Yang P., George C., Wang Y., Schober D.,
RA   Gackenheimer S., Johnson D., Beavers L.S., Gadski R.A., Baez M.;
RT   "Cloning and characterization of Rhesus monkey neuropeptide Y receptor
RT   subtypes(1).";
RL   Peptides 22:343-350(2001).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF303089; AAG40771.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   383 AA;  44306 MW;  F872C45AA90DF62A CRC64;

  Query Match           43.6%;  Score 856.5;  DB 6;  Length 383;
  Best Local Similarity   44.6%;  Pred. No. 3.6e-72;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||           |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|    |:   || || : :|   ||   ||| ||: ||   || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |       |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| |||| ||:::::      |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
              ||:   :::|:
Db        362 TSLK---QASPV 370
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RESULT 12
Q99463
ID   Q99463      PRELIMINARY;      PRT;   290 AA.
AC   Q99463;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Y6 encoding protein.
GN   Y6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97066888; PubMed=8910290;
RA   Matsumoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiho H.,
RA   Togami J., Kimura Y., Okada M., Yamaguchi T.;
RT   "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in
RT   primate species.";
RL   J. Biol. Chem. 271:27217-27220(1996).
DR   EMBL; D86519; BAA13103.1; -.
DR   Genew; HGNC:7959; NPY6R.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ   SEQUENCE   290 AA;  33180 MW;  3ECCDD87001CA8DB CRC64;

  Query Match             29.2%;  Score 573;  DB 4;  Length 290;
  Best Local Similarity   40.5%;  Pred. No. 1.2e-45;
  Matches  106;  Conservative   65;  Mismatches   89;  Indels    2;  Gaps    2;

Qy         21 SKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKA-NVTNLL  79
              :|    : : : | ||      :: :  :|::  :||: ||| |: :  ::: || | |::|
Db         15 TKNNNSAFFYFESCQPPSPALLLLCIAYTVVLIVGLFGNLSLIIIIFKKQRKAQNFTSIL  74

Qy         80 IANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALER 139
              ||||: || |:|::|    | :||:||:||||:|:|:::::::| :|::||| |||  |:||
Db         75 IANLSLSDTLVCVMCIHFTIIYTLMDHWIFGDTMCRLTSYVQSVSISVSIFSLVFTAVER 134

Qy        140 HQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLADKV 199
              :|||:|| |||||:: || || |||: : :||:||  :  | :   :| |   :    :|
Db        135 YQLIVNPRGWKPSVTHAYWGITLIWLFSLLLSIPFFLSYHLTDEPFRNLSLPTDLYTHQV 194

Qy        200 VCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ-GRVFHKGTYSLRAG 258
              | |:||   | ::|| | | || :|||||:|| :|   |:|:  :|  |      |
Db        195 ACVENWPSKKDRLLFTTSLFLLQYFVPLGFILICYLKIVICLRRRNAKVDKKKENEGRLN 254

Qy        259 HMKQVNVVLVVMVVAFAVLWLP 280
                |::| :|: :|| |   |||
Db        255 ENKRINTMLISIVVTFGACWLP 276


RESULT 13
Q8QFM2
ID   Q8QFM2      PRELIMINARY;      PRT;   443 AA.
AC   Q8QFM2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y receptor Y5.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22060921; PubMed=12065655;
RA   Holmberg S.K.S., Mikko S., Boswell T., Zoorob R., Larhammar D.;
RT   "Pharmacological characterization of cloned chicken neuropeptide Y
RT   receptors Y1 and Y5.";
RL   J. Neurochem. 81:462-471(2002).
DR   EMBL; AY040844; AAK83556.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   443 AA;  50044 MW;  EFE9F1A391CC092E CRC64;

  Query Match             24.8%;  Score 487;  DB 13;  Length 443;
  Best Local Similarity   26.7%;  Pred. No. 2.3e-37;
  Matches  115;  Conservative   69;  Mismatches  124;  Indels  122;  Gaps    9;

Qy         26 TPYNFS--EHCQDSV-DVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIAN  82
              |  |||   |  : || |:  |::  |:: :: | :||| ::    ::|:|  : |:|| |
Db         20 TTKNFSAWEDYKSSVDDIQYFLIGLYTLISLAGFVGNLLVLTALTKRKQK-TIINILIGN  78

Qy         83 LAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQL 142
              ||||| |: | | | |    ::| |:||  :| :  |:|| || || | |: :|  |:::
Db         79 LAFSDILVVLFCSPFTLTSVLLDRWMFGTVMCHIMPFLQCTSVLVSTLMLISIAAVRYRM 138

Qy        143 IINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHK----NHSKALEFLADK 198
              :  |      :    |  ||:|| : | :  |          ||||    : :  || | ::
Db        139 VKYPLSSNLTAKHGYFLIVIIWAVGCAICSPL-------PVFHKIVDLHKTLNLEALENR 191

Qy        199 VVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYR----RLQRQGRVFHK---- 250
              ::| ||||   :|  :|  ||| || |||  :   :  : |    ||  :   | :
Db        192 LLCIESWPSDSYRIAFTISLLLMQYILPLVCLTASHTSVCRSVGSRLSSKEGKFQENEMI 251

Qy        251 ----------GTYSLRAGH---------------MKQVNVV------------------- 266
                       || :  : |               |: : |
Db        252 NLTLHPSKSAGTEAQPSSHTSWSCALVRKHHRRYSKKTSTVMPAILRQQQDADFRDLPET 311

Qy        267 ----------------------------------------------------LVVMV 271
                                                                   | |::
Db        312 SGTEKSQLSSSSSKFIPGVPICFEMKPEENTEIQDMITVSQSIIRIKTRSRRVFCRLTVLI 371

Qy        272 VAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKK 331
              : |   |:|||:|: : |::   |   |  |:: :|||| | | |:|| :|||| : |
Db        372 LVFGFSWMPLHLFHIVTDFNATLISNRHFKLVYCICHLLGMMSCCLNPILYGFLNNSIKA 431

Qy        332 EIKALVLTCQ 341
              :: :|:  ||
Db        432 DLMSLIPCCQ 441


RESULT 14
Q8BWV1
ID   Q8BWV1      PRELIMINARY;      PRT;   381 AA.
AC   Q8BWV1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neuropeptide Y receptor type 2.
GN   NPY2R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
```

```
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK049892; BAC33975.1; -.
DR   MGD; MGI:108418; Npy2r.
DR   GO; GO:0001601; F:peptide YY receptor activity; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR001220; Lectin_legB.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
SQ   SEQUENCE   381 AA;  42628 MW;  90787C051347884A CRC64;

  Query Match             24.0%;  Score 471;  DB 11;  Length 381;
  Best Local Similarity   32.5%;  Pred. No. 6.4e-36;
  Matches  122;  Conservative   67;  Mismatches  148;  Indels   38;  Gaps   10;

Qy         15 PQGENRSKPLG-TPYNFSEHCQDS---VDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQK 70
              | |    : | |   | :        ||    |:| | :: :|     ::||:||  :: | :: |
Db         20 PYGPGHTTPRGELPPDPEPELIDSTKLVEVQVILILAYCSIILLGVVGNSLVIHVVIKFK 79

Qy         71 EKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSIL 130
                 |||  ||||| :| |:  || | |  ||:|  |  |  || :  : | ::| || :
Db         80 SMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHLVPYAQGLAVQVSTI 139

Qy        131 SLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLP---FLANSILENVFHKN 187
              :| ::||:||: |:      | |   ::| | | | |: :|: |    |   |::| :
Db        140 TLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAIFREYSLIEII---- 195

Qy        188 HSKALEFLADKVVCTESWP---LAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
                :|  : | ||| ||    : : |:|:   ||  | |||| |   | ||: :|:
Db        196 ----PDF--EIVACTEKWPGEEKSVYGTVYSLSTLLILYVLPLGIISFSYTRIWSKLRNH 249

Qy        245 GRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIF 304
                    : : |  ::  :|| :|| ||| ||||| |     |      : :    |||
Db        250 VSPGAASDHYHQRRH--KMTKMLVCVVVVFAVSWLPLHAFQLAVDIDSHVLDLKEYKLIF 307

Qy        305 LVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVS-- 362
               | |::|| ||  f| :||::|:|::|   :    |:|           |  :|:|||
Db        308 TVFHIIAMCSTFANPLLYGWMNSNYRKAFLS-AFRCEQR----------LDAIHSEVSMT 356

Qy        363 ---KGSLRLSGRSNP 374
                 | :| :   : |
Db        357 PKAKKNLEVKKNNGP 371


RESULT 15
Q9ERC0
ID   Q9ERC0      PRELIMINARY;      PRT;   381 AA.
AC   Q9ERC0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide Y/peptide YY-Y2 receptor.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Small intestine;
RA   Voisin T., Goumain M., LaBurthe M.;
RT   "Cloning of a cDNA encoding a rat type 2 neuropeptide Y/peptide YY
RT   receptor expressed in intestinal epithelial crypt cells.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY004257; AAF89094.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR001220; Lectin_legB.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
KW   Receptor.
SQ   SEQUENCE   381 AA;  42510 MW;  659327904B288BC7 CRC64;

  Query Match             23.9%;  Score 469;  DB 11;  Length 381;
  Best Local Similarity   32.4%;  Pred. No. 9.8e-36;
  Matches  125;  Conservative   63;  Mismatches  132;  Indels   66;  Gaps   12;

Qy         12 PKSPQGENRSKPLGTPYNFSEHCQDS---VDVMVFIVTSYSIETVVGVLGNLCLMCVTVR 68
              | :|:||        | :       ||   |:| | :: :|     ::||:||  :: | ::
Db         25 PTTPRGE-------LPPDPEPELIDSTKLVEVQVVLILAYCSIILLGVVGNSLVIHVVIK 77

Qy         69 QKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVS 128
              |    |||  ||||| :| |:  || | |  ||:|  |  |  || :  : | ::| ||
Db         78 FKSMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHLVPYAQGLAVQVS 137

Qy        129 ILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLP---FLANSILENVFH 185
                 ::| ::||:||: |:      | |   ::| | | | :: :|: |    |   |::| :
Db        138 TITLTVIALDRHRCIVYHLESKISKQISFLIIGLAWGVSALLASPLAIFREYSLIEII-- 195

Qy        186 KNHSKALEFLADKVVCTESWP---LAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQ 242
                    :|  : | ||| ||    : : |:|:   ||  | |||| |   | ||: :|:
Db        196 ------PDF--EIVACTEKWPGEEKSVYGTVYSLSTLLILYVLPLGIISFSYTRIWSKLK 247

Qy        243 ------------RQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDW 290
                         | |  || |              :|| :|| ||| ||||| |     |
Db        248 NHVSPGAASDHYHQRR--HKTT------------KMLVCVVVVFAVSWLPLHAFQLAVDI 293

Qy        291 HHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESE 350
                 : :    ||| | |::|| ||  || :||::|:|::|    :     |:|
Db        294 DSHVLDLKEYKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAFLS-AFRCEQR------- 345

Qy        351 HLPLSTVHTEVS---KGSLRLSGRSN 373
                | :|:|||   |     |  : |
Db        346 ---LDAIHSEVSMTFKAKKNLEVKKN 368


Search completed: May 11, 2004, 12:56:56
Job time : 48 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:37 ; Search time 23 Seconds
(without alignments)
841.728 Million cell updates/sec

Title: US-09-430-775-2
Perfect score: 1965
Sequence: 1 MNTSHLLALLLPKSPQGENR.....TVHTEVSKGSLRLSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1965	100.0	375	1	US-08-176-412-2	Sequence 2, Appli
2	1965	100.0	375	2	US-08-555-268A-2	Sequence 2, Appli
3	1965	100.0	375	2	US-08-495-695B-2	Sequence 2, Appli
4	1965	100.0	375	4	US-09-200-673-17	Sequence 17, Appl
5	1965	100.0	375	5	PCT-US94-14436-2	Sequence 2, Appli
6	1839	93.6	350	2	US-08-495-695B-33	Sequence 33, Appl
7	1492	75.9	375	2	US-08-495-695B-28	Sequence 28, Appl
8	1492	75.9	375	5	PCT-US94-14436-28	Sequence 28, Appl
9	1412	71.9	350	2	US-08-495-695B-32	Sequence 32, Appl
10	869	44.2	382	2	US-08-555-268A-13	Sequence 13, Appl
11	867	44.1	382	1	US-08-415-818-7	Sequence 7, Appli
12	867	44.1	382	2	US-08-894-236-7	Sequence 7, Appli
13	867	44.1	382	2	US-08-555-268A-14	Sequence 14, Appl
14	867	44.1	382	5	PCT-US96-01444-7	Sequence 7, Appli
15	863	43.9	371	1	US-08-415-818-6	Sequence 6, Appli
16	863	43.9	371	2	US-08-894-236-6	Sequence 6, Appli
17	863	43.9	371	2	US-08-919-624-4	Sequence 4, Appli
18	863	43.9	371	5	PCT-US96-01444-6	Sequence 6, Appli
19	860.5	43.8	384	4	US-09-200-673-15	Sequence 15, Appl
20	856.5	43.6	383	3	US-09-045-186-2	Sequence 2, Appli
21	856.5	43.6	384	1	US-08-232-144-4	Sequence 4, Appli
22	856.5	43.6	384	2	US-08-555-268A-15	Sequence 15, Appl
23	856.5	43.6	384	4	US-10-013-846-4	Sequence 4, Appli
24	856.5	43.6	384	5	PCT-US93-05039-3	Sequence 3, Appli
25	854.5	43.5	411	3	US-08-817-869-3	Sequence 3, Appli
26	854.5	43.5	411	5	PCT-US95-14377-3	Sequence 3, Appli
27	823.5	41.9	370	1	US-08-415-818-12	Sequence 12, Appl
28	823.5	41.9	370	2	US-08-894-236-12	Sequence 12, Appl
29	823.5	41.9	370	5	PCT-US96-01444-12	Sequence 12, Appl
30	705.5	35.9	301	1	US-08-118-270-72	Sequence 72, Appl
31	705.5	35.9	301	5	PCT-US93-08528-72	Sequence 72, Appl
32	618.5	31.5	228	3	US-08-513-974B-313	Sequence 313, App
33	618.5	31.5	228	3	US-08-513-974B-362	Sequence 362, App
34	618.5	31.5	228	3	US-08-776-971-130	Sequence 130, App
35	556.5	28.3	394	4	US-10-013-846-17	Sequence 17, Appl
36	487.5	24.8	370	3	US-09-172-353-2	Sequence 2, Appli
37	487.5	24.8	370	3	US-09-172-353-3	Sequence 3, Appli
38	487.5	24.8	370	4	US-09-799-955-2	Sequence 2, Appli
39	487.5	24.8	370	4	US-09-799-955-3	Sequence 3, Appli
40	485.5	24.7	370	3	US-08-513-974B-26	Sequence 26, Appl
41	485.5	24.7	370	3	US-08-513-974B-323	Sequence 323, App
42	485.5	24.7	370	3	US-09-172-353-5	Sequence 5, Appli
43	485.5	24.7	370	3	US-08-776-971-21	Sequence 21, Appl
44	485.5	24.7	370	3	US-08-776-971-104	Sequence 104, App
45	485.5	24.7	370	4	US-09-799-955-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-08-176-412-2
; Sequence 2, Application US/08176412
; Patent No. 5516653
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/176,412
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743/JPW/TEP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-176-412-2

  Query Match           100.0%;  Score 1965;  DB 1;  Length 375;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-144;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
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Db        361 VSKGSLRLSGRSNPI 375


RESULT 2
US-08-555-268A-2
; Sequence 2, Application US/08555268A
; Patent No. 5958709
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/555,268A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-Z/JPW/MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0526
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-555-268A-2

  Query Match           100.0%;  Score 1965;  DB 2;  Length 375;
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  Best Local Similarity   100.0%;  Pred. No. 5.2e-144;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
                 |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375


RESULT 3
US-08-495-695B-2
; Sequence 2, Application US/08495695B
; Patent No. 5976814
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/495,695B
;      FILING DATE:  13-Jan-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-A-PCT-US/JPW/JHB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  protein
US-08-495-695B-2

  Query Match             100.0%;  Score 1965;  DB 2;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-144;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375


RESULT 4
US-09-200-673-17
; Sequence 17, Application US/09200673A
; Patent No. 6316203
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT: Weinshank, Richard L.
;  APPLICANT: Walker, Mary W.
;  APPLICANT: Branchek, Theresa
;  TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
;  TITLE OF INVENTION: in Such Methods, and DNA Encoding A Hypothalamic
;  TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)
;  FILE REFERENCE: 46166-BZ/JPW
;  CURRENT APPLICATION NUMBER: US/09/200,673A
;  CURRENT FILING DATE: 1998-11-25
;  EARLIER APPLICATION NUMBER: 08/566,096
;  EARLIER FILING DATE: 1995-12-01
;  EARLIER APPLICATION NUMBER: 08/349,025
;  EARLIER FILING DATE: 1994-12-02
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-200-673-17

  Query Match             100.0%;  Score 1965;  DB 4;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-144;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375


RESULT 5
PCT-US94-14436-2
; Sequence 2, Application PC/TUS9414436
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14436
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-A-PCT\JPW\MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  375 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US94-14436-2

  Query Match             100.0%;  Score 1965;  DB 5;  Length 375;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-144;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
              |||||||||||||||
Db        361 VSKGSLRLSGRSNPI 375
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Qy          61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy         121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy         181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy         241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy         301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy         361 VSKGSLRLSGRSNPI 375
               |||||||||||||||
Db         361 VSKGSLRLSGRSNPI 375
```

RESULT 6
US-08-495-695B-33
; Sequence 33, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,695B
; FILING DATE: 13-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-495-695B-33

Query Match 93.6%; Score 1839; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.4e-134;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 MNTSHLLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MNTSHLLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60

Qy          61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy         121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180

Qy         181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240

Qy         241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300

Qy         301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESE 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESE 350
```

RESULT 7
US-08-495-695B-28
; Sequence 28, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,695B
; FILING DATE: 13-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-495-695B-28

Query Match 75.9%; Score 1492; DB 2; Length 375;
Best Local Similarity 75.1%; Pred. No. 1.4e-107;
Matches 280; Conservative 34; Mismatches 59; Indels 0; Gaps 0;

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Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||:| | |   ||:| : || : || |: |||| |:: ||:|:||:|||:||||||
Db          1 MNTSHLMASLSPAFLQGKNGTNPLDSLYNLSDGCQDSADLLAFIITTYSVETVLGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:|||||||||||||||||:|||||  |||||||||| ||||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||||||||||||:|| |:| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVVIWFISCFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| ||||| || ||| ||||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCVPLAFILVCYMRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| | ||  | | | | || :| :|: || |||||||||||||:|||: |||| |||
Db        241 LQRQRRAFHTHTCSSRVGQMKPINGMLMAMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:||| |||||||||||||||| ||||:|||||||:   | | | ||||||||:
Db        301 NLIFLMCHLFAMASTCVNPFIYGFLNINFKKDIKALVLTCRCRPPQGEPEPLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373
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RESULT 8
PCT-US94-14436-28
; Sequence 28, Application PC/TUS9414436
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14436
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT\JPW\MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14436-28

Query Match 75.9%; Score 1492; DB 5; Length 375;
Best Local Similarity 75.1%; Pred. No. 1.4e-107;
Matches 280; Conservative 34; Mismatches 59; Indels 0; Gaps 0;

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Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||:| | |   ||:| : || : || |: |||| |:: ||:|:||:|||:||||||
Db          1 MNTSHLMASLSPAFLQGKNGTNPLDSLYNLSDGCQDSADLLAFIITTYSVETVLGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:|||||||||||||||||:|||||  |||||||||| ||||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||||||||||||:|| |:| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVVIWFISCFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| ||||| || ||| ||||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCVPLAFILVCYMRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| | ||  | | | | || :| :|: || |||||||||||||:|||: |||| |||
Db        241 LQRQRRAFHTHTCSSRVGQMKPINGMLMAMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:||| |||||||||||||||| ||||:|||||||:   | | | ||||||||:
Db        301 NLIFLMCHLFAMASTCVNPFIYGFLNINFKKDIKALVLTCRCRPPQGEPEPLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373
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RESULT 9
US-08-495-695B-32
; Sequence 32, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,695B
; FILING DATE: 13-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-495-695B-32

  Query Match             71.9%;  Score 1412;  DB 2;  Length 350;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-101;
  Matches  265;  Conservative   30;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||:| | |   ||:| : || : || |: |||| |:: ||:|:||:|||:||||||
Db          1 MNTSHLMASLSPAFLQGKNGTNPLDSLYNLSDGCQDSADLLAFIITTYSVETVLGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:|||||||||||||||||:|||||  |||||||||||| ||||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||||||||||||:|| |:| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVVIWFISCFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| |||||  ||   ||| ||||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCVPLAFILVCYMRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| | ||  | | | | ||::| :|: || |||||||||||||:|||: |||| |||
Db        241 LQRQRRAFHTHTCSSRVGQMKRINGMLMAMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESE 350
              |||||:||| |||||||||||||| ||||:||||||:   |  | |
Db        301 NLIFLMCHLFAMASTCVNPFIYGFLNINFKKDIKALVLTCRCRPPQGEPE 350


RESULT 10
US-08-555-268A-13
; Sequence 13, Application US/08555268A
; Patent No. 5958709
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/555,268A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  44743-Z/JPW/MAT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0526
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  382 amino acids
;      TYPE:  amino acid
;
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-555-268A-13

  Query Match             44.2%;  Score 869;  DB 2;  Length 382;
  Best Local Similarity   46.8%;  Pred. No. 1.4e-59;
  Matches  168;  Conservative   74;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:          |   : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db         16 YNVSENSPFLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              ||||||||| ||:|:   ||:|| :|||:|   ||||:   || :  :| | |   |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:  :  |   | |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::||:|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| || |||
Db        254 SSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              ||| ||||| ||:::::     |   :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 11
US-08-415-818-7
; Sequence 7, Application US/08415818
; Patent No. 5621079
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/415,818
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
```

```
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  382 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-415-818-7

  Query Match             44.1%;  Score 867;  DB 1;  Length 382;
  Best Local Similarity   46.5%;  Pred. No. 2e-59;
  Matches  167;  Conservative   75;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:          |   : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db         16 YNASENSPLLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              |||||||||  ||:|:    ||:|| :|||:|   ||||:   ||  :   :| |  |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:  :  |   | |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| || |||
Db        254 SSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::     |   :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 12
US-08-894-236-7
; Sequence 7, Application US/08894236
; Patent No. 5939263
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/894,236
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,818
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  382 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-894-236-7

  Query Match             44.1%;  Score 867;  DB 2;  Length 382;
  Best Local Similarity   46.5%;  Pred. No. 2e-59;
  Matches  167;  Conservative   75;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:          |   : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db         16 YNASENSPLLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              |||||||||  ||:|:    ||:|| :|||:|   ||||:   ||  :   :| |  |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:  :  |   | |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| || |||
Db        254 SSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::     |   :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 13
US-08-555-268A-14
; Sequence 14, Application US/08555268A
; Patent No. 5958709
;  GENERAL INFORMATION:
;    APPLICANT:  Bard, Jonathan A.
;    APPLICANT:  Walker, Mary
;    APPLICANT:  Branchek, Theresa
;    APPLICANT:  Weinshank, Richard L.
;    TITLE OF INVENTION:  DNA ENCODING A HUMAN NEUROPEPTIDE
;    TITLE OF INVENTION:  Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
;    TITLE OF INVENTION:  RECEPTOR (Y4) AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/555,268A
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  White, John P.
;       REGISTRATION NUMBER:  28,678
;       REFERENCE/DOCKET NUMBER:  44743-Z/JPW/MAT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 278-0400
;       TELEFAX:  (212) 391-0526
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  382 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-555-268A-14

  Query Match             44.1%;  Score 867;  DB 2;  Length 382;
  Best Local Similarity   46.5%;  Pred. No. 2e-59;
  Matches  167;  Conservative   75;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
              || ||:          |  : |:  :  :|    ::|| ||| |: : ::|||  ||||
Db         16 YNASENSPLLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              ||||||||| ||:|:   ||:|| :|||:|   ||||:   || :   :| |  |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:  :  |    | |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| || |||
Db        254 SSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::     |  :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 14
PCT-US96-01444-7
; Sequence 7, Application PC/TUS9601444
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
;    TITLE OF INVENTION:  NEUROPEPTIDE Y RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mary A. Appollina
;      STREET:  P.O. Box 2000, 126 E. Lincoln Ave.
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01444
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/383,746
;      FILING DATE:  03-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/415,818
;      FILING DATE:  03-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19390Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3462
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  382 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US96-01444-7

  Query Match             44.1%;  Score 867;  DB 5;  Length 382;
  Best Local Similarity   46.5%;  Pred. No. 2e-59;
  Matches  167;  Conservative   75;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
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Db         16 YNASENSPLLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
              :|| ||:||| |: ::| | | |||:||:|:||||:||:: |:||:|:|||| ||||:|:
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
              ||||||||| ||:|:   ||:|| :|||:|   ||||:   || :   :| |  |    |
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
              | || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:  :  |    | |
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253

Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
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Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
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Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 15
US-08-415-818-6
; Sequence 6, Application US/08415818
; Patent No. 5621079
;  GENERAL INFORMATION:
;    APPLICANT:  Cascieri, Margaret A.
;    APPLICANT:  Linemeyer, David L.
;    APPLICANT:  MacNeil, Douglas J.
;    APPLICANT:  Shiao, Lin-Lin
;    APPLICANT:  Strader, Catherine D.
;    APPLICANT:  Tan, Carina P.
;    APPLICANT:  Weinberg, David H.
```

; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,818
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-415-818-6

Query Match 43.9%; Score 863; DB 1; Length 371;
Best Local Similarity 43.2%; Pred. No. 3.9e-59;
Matches 156; Conservative 89; Mismatches 108; Indels 8; Gaps 5;

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Qy          71 EKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSIL 130
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Db         126 SLVLIAIERYQLIVNPRGWKPRVAHAYWGIILIWLISLTLSIPLFLSYHLTNEPFH-NLS 184

Qy         190 KALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGR-VF 248
                  :    :| | | ||   :: :::| | : || :|||||:|| :|   |::: | |
Db         185 LPTDIYTHQVACVEIWPSKLNQLLFSTSLFMLQYFVPLGFILICYLKIVLCLRKRTRQVD 244

Qy         249 HKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCH 308
                :     |    |:|||:|: :|| |   ||||::|| : ||:|| :  || :|:|:|||
Db         245 RRKENKSRLNENKRVNVMLISIVVTFGACWLPLNIFNVIFDWYHEMLMSCHHDLVFVVCH 304

Qy         309 LLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRL 368
               |:|| |||:||  ||||| ||:|::  |:  |    | |  |:: :||:||: |||||:|
Db         305 LIAMVSTCINPLFYGFLNKNFQKDLMMLIHHCWCGEPQESYENIAMSTMHTDESKGSLKL 364

Qy         369 S 369
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Db         365 A 365
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Search completed: May 11, 2004, 12:58:03
Job time : 24 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 12:55:33 ; Search time 48 Seconds
(without alignments)
2168.490 Million cell updates/sec

Title: US-09-430-775-2
Perfect score: 1965
Sequence: 1 MNTSHLLALLLPKSPQGENR.....TVHTEVSKGSLRLSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1965	100.0	375	9	US-09-962-646-17	Sequence 17, Appl
2	1965	100.0	375	12	US-10-181-906-12	Sequence 12, Appl
3	1965	100.0	375	14	US-10-225-567A-203	Sequence 203, App
4	1519	77.3	375	12	US-10-081-810-47	Sequence 47, Appl
5	1494	76.0	375	12	US-10-081-810-48	Sequence 48, Appl
6	960	48.9	375	12	US-10-081-810-51	Sequence 51, Appl
7	922	46.9	374	12	US-10-072-012-359	Sequence 359, App
8	869	44.2	382	9	US-09-771-956-3	Sequence 3, Appli
9	867.5	44.1	383	12	US-10-081-810-50	Sequence 50, Appl
10	863	43.9	371	15	US-10-328-916-9	Sequence 9, Appli
11	860.5	43.8	384	9	US-09-962-646-15	Sequence 15, Appl
12	856.5	43.6	384	9	US-09-771-956-2	Sequence 2, Appli
13	856.5	43.6	384	10	US-09-393-696-23	Sequence 23, Appl
14	856.5	43.6	384	12	US-10-410-648-4	Sequence 4, Appli
15	856.5	43.6	384	14	US-10-013-846-4	Sequence 4, Appli
16	856.5	43.6	384	14	US-10-176-847-26	Sequence 26, Appl
17	856.5	43.6	384	14	US-10-225-567A-378	Sequence 378, App
18	856.5	43.6	384	14	US-10-309-515-10	Sequence 10, Appl
19	856.5	43.6	384	14	US-10-177-293-330	Sequence 330, App
20	856.5	43.6	384	14	US-10-060-369-10	Sequence 10, Appl
21	856.5	43.6	384	14	US-10-291-990-31	Sequence 31, Appl
22	856.5	43.6	384	14	US-10-126-764-10	Sequence 10, Appl
23	856.5	43.6	384	15	US-10-295-027-640	Sequence 640, App
24	856.5	43.6	384	15	US-10-295-027-746	Sequence 746, App
25	847	43.1	371	12	US-10-081-810-49	Sequence 49, Appl
26	846.5	43.1	388	12	US-10-181-906-6	Sequence 6, Appli
27	842.5	42.9	384	14	US-10-274-851-4	Sequence 4, Appli
28	603	30.7	227	13	US-10-044-592-69	Sequence 69, Appl
29	573	29.2	290	12	US-10-181-906-16	Sequence 16, Appl
30	573	29.2	290	14	US-10-225-567A-376	Sequence 376, App
31	561.5	28.6	383	9	US-09-771-956-27	Sequence 27, Appl
32	560.5	28.5	383	9	US-09-771-956-21	Sequence 21, Appl
33	557	28.3	395	9	US-09-771-956-25	Sequence 25, Appl
34	556.5	28.3	394	9	US-09-771-956-10	Sequence 10, Appl
35	556.5	28.3	394	12	US-10-410-648-17	Sequence 17, Appl
36	556.5	28.3	394	14	US-10-013-846-17	Sequence 17, Appl
37	538.5	27.4	394	14	US-10-274-851-17	Sequence 17, Appl
38	529	26.9	352	9	US-09-771-956-23	Sequence 23, Appl
39	522	26.6	341	9	US-09-771-956-26	Sequence 26, Appl
40	518	26.4	341	9	US-09-771-956-20	Sequence 20, Appl
41	517	26.3	508	9	US-09-771-956-22	Sequence 22, Appl
42	515	26.2	350	9	US-09-771-956-6	Sequence 6, Appli
43	506	25.8	499	9	US-09-771-956-9	Sequence 9, Appli
44	498	25.3	499	9	US-09-771-956-24	Sequence 24, Appl
45	485.5	24.7	370	13	US-10-044-592-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-962-646-17
; Sequence 17, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION:
; APPLICANT: GERALD, CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHEK, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPT
; FILE REFERENCE: 1795/46166BZA
; CURRENT APPLICATION NUMBER: US/09/962,646
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/200,673
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566,096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349,025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-962-646-17

Query Match 100.0%; Score 1965; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.8e-170;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360

Qy        361 VSKGSLRLSGRSNPI 375
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Db        361 VSKGSLRLSGRSNPI 375


RESULT 2
US-10-181-906-12
; Sequence 12, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
;  APPLICANT: Karsenty, Gerard
;  APPLICANT:  Amling , Michael
;  APPLICANT:  Ducy, Patricia
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
;  TITLE OF INVENTION:  MODULATION OF NEUROPEPTIDE Y ACTIVITY
;  FILE REFERENCE: 9142-020-999
;  CURRENT APPLICATION NUMBER: US/10/181,906
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/US01/02040
;  PRIOR FILING DATE: 2001-01-22
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-181-906-12

  Query Match            100.0%;  Score 1965;  DB 12;  Length 375;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-170;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
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Db         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
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Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
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Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
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Db        361 VSKGSLRLSGRSNPI 375


RESULT 3
US-10-225-567A-203
; Sequence 203, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-203

  Query Match            100.0%;  Score 1965;  DB 14;  Length 375;
  Best Local Similarity  100.0%;  Pred. No. 5.8e-170;
  Matches  375;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
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Qy        361 VSKGSLRLSGRSNPI 375
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Db        361 VSKGSLRLSGRSNPI 375


RESULT 4
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; Sequence 47, Application US/10081810
; Publication No. US20030064438A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODIES
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: D0132 NP
;  CURRENT APPLICATION NUMBER: US/10/081,810
;  CURRENT FILING DATE:  2002-02-22
```

```
;  PRIOR APPLICATION NUMBER: US 60/270,793
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/270,792
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/296,427
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-081-810-47

  Query Match           77.3%;  Score 1519;  DB 12;  Length 375;
  Best Local Similarity  75.9%;  Pred. No. 1.8e-129;
  Matches  283;  Conservative   35;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||| || | | | ||:| : || :|||||: |||| ::: ||:|:|||||::|||||
Db          1 MNTSHFLAPLFPGSLQGKNGTNPLDSPYNFSDGCQDSAELLAFIITTYSIETILGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || |||||:||||||||||||||||:|||||  ||||||||||| |||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||| |||||||:|| |:| |||||||||| |
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSIFQAYLGIVVIWFISCFLSLPFLANSTL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| ||||| ||   ||| ||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCIPLAFILVCYIRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              ||||  |||    | ||| ||::| :|: || |||||||||||:||||: |||| |||
Db        241 LQRQKHVFHAHACSSRAGQMKRINSMLMTMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:|||||||||||||||||| ||||:|||||||   :|  ||||||||||||:
Db        301 NLIFLMCHLLAMASTCVNPFIYGFLNINFKKDIKALVLTCHCRSPQGESEHLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373


RESULT 5
US-10-081-810-48
; Sequence 48, Application US/10081810
; Publication No. US20030064438A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODIE
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: D0132 NP
;  CURRENT APPLICATION NUMBER: US/10/081,810
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: US 60/270,793
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/270,792
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/296,427
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-081-810-48

  Query Match           76.0%;  Score 1494;  DB 12;  Length 375;
  Best Local Similarity  75.1%;  Pred. No. 3.3e-127;
  Matches  280;  Conservative   35;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              ||||||:| | |   ||:| : || : || |: |||| |:: ||:|:||:|||:||||||
Db          1 MNTSHLMASLSPAFLQGKNGTNPLDSLYNLSDGCQDSADLLAFIITTYSVETVLGVLGNL 60

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: || ||||||:|||||||||||||||||:|||||  |||||||||| ||||  ||
Db         61 CLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFI 120

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              |||||||||||||||||||||||||||||||||||||||||||||||:|| |:| ||||||||||
Db        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVVIWFISCFLSLPFLANSIL 180

Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
               ::|| |||| :||| ||||| ||   ||| ||||||||||:|| |||||| |||:|
Db        181 NDLFHYNHSKVVEFLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCVPLAFILVCYMRIYQR 240

Qy        241 LQRQGRVFHKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHG 300
              |||| | ||  | | | | ||::| :|: || ||||||||||||:|||: |||| |||
Db        241 LQRQRRAFHTHTCSSRVGQMKRINGMLMAMVTAFAVLWLPLHVFNTLEDWYQEAIPACHG 300

Qy        301 NLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTE 360
              |||||:||| ||||||||||||||| ||||:||||||:    | | | ||||||||:
Db        301 NLIFLMCHLFAMASTCVNPFIYGFLNINFKKDIKALVLTCRCRPPQGEPEPLPLSTVHTD 360

Qy        361 VSKGSLRLSGRSN 373
              :||||:|:  :||
Db        361 LSKGSMRMGSKSN 373


RESULT 6
US-10-081-810-51
; Sequence 51, Application US/10081810
; Publication No. US20030064438A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODIES
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: D0132 NP
;  CURRENT APPLICATION NUMBER: US/10/081,810
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: US 60/270,793
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/270,792
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/296,427
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Danio rerio
US-10-081-810-51

  Query Match           48.9%;  Score 960;  DB 12;  Length 375;
  Best Local Similarity  50.1%;  Pred. No. 1e-78;
  Matches  188;  Conservative   57;  Mismatches  112;  Indels   18;  Gaps    3;

Qy          1 MNTSHLLALLLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNL 60
              |  |||           | |  |  |     |  |:    |:: :||    ||::||
Db          1 MERSHL-----------NNSSWLLEDP-----TCPASLSSTTFLIVAYSTMLAVGLVGNT 44

Qy         61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
              ||: |  ||||  ||||: | ||: || |:||:| |:| :||:||  || || |||:: |:
Db         45 CLVVVITRQKEMRNVTNIFIVNLSCSDILVCLVCLPVTIIYTLMDRWILGEALCKVTPFV 104

Qy        121 QCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
              ||||||||| |:||:|||||||||:|||||| :  :|| : :||:||| :|||||: :||
Db        105 QCMSVTVSIFSMVLIALERHQLIIHPTGWKPVVRHSYLAVAVIWIIACFISLPFLSFNIL 164
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Qy        181 ENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRR 240
Db        165 TNSPFHNLSLPFNPFSDHFICIEQWPSEGNRLTYTTTLLLCQYCLPLALILVCYFRIFLR 224

Qy        241 LQRQGRVFH--KGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPIC 298
Db        225 LSRRKDMVERARGGRQKKAKGSKRVNAMLASIVAAFALCWLPLNVFNTIFDWNHEAIPVC 284

Qy        299 HGNLIFLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVH 358
Db        285 QHDAIFSACHLTAMASTCVNPVIYGFLNNNFQKELKSLLSRCRCWGPAESYESFPLSTVS 344

Qy        359 TEVSKGSLRLSGRSN 373
Db        345 TGITKGSILSNGSAS 359
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RESULT 7
US-10-072-012-359
; Sequence 359, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 359
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Gadus morhua
US-10-072-012-359

  Query Match             46.9%;  Score 922;  DB 12;  Length 374;
  Best Local Similarity   51.3%;  Pred. No. 2.8e-75;
  Matches  178;  Conservative   62;  Mismatches   95;  Indels   12;  Gaps    4;

Qy         32 EHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMC 91
Db         28 EECPSSKSGTTFLILVYSTMIAVGIVGNSCLVFVIARQKEMHNVTNIFIANLSCSDILMC 87

Qy         92 LLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKP 151
Db         88 IFCLPVTLIYTLMDRWILGEALCKLTPFVQCISVTVSIFSLVLIAMERYQLIIHPTGWKP 147

Qy        152 SISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLA-DKVVCTESWPLAHH 210
Db        148 MVGQSYMAVGIIWVVACLISVPFLSFTVLDNLPLQNLS--LPFPGQDHWLCTESWPTNSN 205

Qy        211 RTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYSLRAGHMK---QVNVVL 267
Db        206 RLAYTTSLLVFQYFLPLGLIAACYLSIFLRLRRRKDMVERARDSSRDNRAKGSRRINVML 265

Qy        268 VVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFIYGFLNT 327
Db        266 GSIVALFAVCWLPLNIFNTVFDWHHELMVSCQHNLIFSVCHLVAMASTCVNPVVYGFLNS 325

Qy        328 NFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEV------SKGSLRL 368
Db        326 NFQKQLKATLSHCRCWGAAERYENLPLSAVSTEVTKESHMSKGSISI 372
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RESULT 8
US-09-771-956-3
; Sequence 3, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
;  APPLICANT:  Bennett, Michele
;  APPLICANT:  Brodbeck, Robbin
;  APPLICANT:  Krause, James
;  TITLE OF INVENTION:  Chimeric Neuropeptide Y Receptors
;  FILE REFERENCE:  N2000.001
;  CURRENT APPLICATION NUMBER: US/09/771,956
;  CURRENT FILING DATE:  2001-01-29
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 382
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-771-956-3

  Query Match             44.2%;  Score 869;  DB 9;  Length 382;
  Best Local Similarity   46.8%;  Pred. No. 1.9e-70;
  Matches  168;  Conservative   74;  Mismatches  101;  Indels   16;  Gaps    4;

Qy         28 YNFSEH----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTN 77
Db         16 YNVSENSPFLAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTN 75

Qy         78 LLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVAL 137
Db         76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCVSITVSIFSLVLIAV 135

Qy        138 ERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKNHSKALEFLAD 197
Db        136 ERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTDEPFQNVS--LAAFKD 193

Qy        198 KVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGRVFHKGTYS-LR 256
Db        194 KYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYR 253
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Qy        257 AGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCHLLAMASTC 316
              :   |::||:|: :|||||| |||| :||:: ||:|: |  |: ||:||:||| || |||
Db        254 SSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTC 313

Qy        317 VNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRLSGRSNPI 375
              |||  ||||| ||:::::     |   :  :: | : :||:||:||| ||:   :::|:
Db        314 VNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369


RESULT 9
US-10-081-810-50
; Sequence 50, Application US/10081810
; Publication No. US20030064438A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODIE
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: D0132 NP
;  CURRENT APPLICATION NUMBER: US/10/081,810
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: US 60/270,793
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/270,792
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: US 60/296,427
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Cavia porcellus
US-10-081-810-50

  Query Match             44.1%;  Score 867.5;  DB 12;  Length 383;
  Best Local Similarity   45.4%;  Pred. No. 2.6e-70;
  Matches  169;  Conservative   76;  Mismatches  106;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSEH-----------CQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |      || ||             |   : |:  :  :|    ::|| ||| |:
Db          8 QLENHS----VHYNLSEEKPSFFAPENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIL 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:|||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWIFGEIMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||| ||:|:   ||:|| :|||:|   ||||:   :| :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYIGIAVIWVLAVASSLPFMIYQVLTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|    |:   ||:|| : :|   ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAFKDKLVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHKGTYS-LRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |   |  |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDSKYRSSESKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| ||||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
              ||:   :::|:
Db        362 TSLK---QASPL 370


RESULT 10
US-10-328-916-9
; Sequence 9, Application US/10328916
; Publication No. US20040002114A1
; GENERAL INFORMATION:
;  APPLICANT: Gregoire, Francine M.
;  APPLICANT:  Johnson, Jeffrey D.
;  APPLICANT:  Blume, John E.
;  APPLICANT:  Metabolex, Inc.
;  TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
;  TITLE OF INVENTION:  Involved in Islet Cell Signaling
;  FILE REFERENCE: 016325-007210US
;  CURRENT APPLICATION NUMBER: US/10/328,916
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US 60/345,697
;  PRIOR FILING DATE: 2002-01-04
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 371
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: mouse pancreatic polypeptide receptor type 2 (PP2)
US-10-328-916-9

  Query Match             43.9%;  Score 863;  DB 15;  Length 371;
  Best Local Similarity   43.2%;  Pred. No. 6.3e-70;
  Matches  156;  Conservative   89;  Mismatches  108;  Indels    8;  Gaps    5;

Qy         12 PKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTV-RQK 70
              |    |:: :    : : : | ||     :: :: :|:: ::|: ||| |: :   :|:
Db         10 PNKTSGKSNN----SAFFYFESCQPPFLAILLLLIAYTVILIMGIFGNLSLIIIIFKKQR 65

Qy         71 EKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSIL 130
              |  ||||:|||||: || |:|::| | | :||:||:|:|| |:||:::::| :||:|||
Db         66 EAQNVTNILIANLSLSDILVCVMCIPFTVIYTLMDHWVFGNTMCKLTSYVQSVSVSVSIF 125

Qy        131 SLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLP-FLANSILENVFHKNHS 189
              ||||:|:||:|||:|| |||| :: || ||:|||:|:  ||:| ||:  :    || | |
Db        126 SLVLIAIERYQLIVNPRGWKPRVAHAYWGIILIWLISLTLSIPLFLSYHLTNEPFH-NLS 184

Qy        190 KALEPLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQGR-VF 248
              :    :| | | ||   :: :::| | : || :||||||:|| :|   |::: | |
Db        185 LPTDIYTHQVACVEIWPSKLNQLLFSTSLFMLQYFVPLGFILICYLKIVLCLRKRTRQVD 244

Qy        249 HKGTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLIFLVCH 308
              :     |    |:|||:|: :|| |   ||||::|| : ||:|| :  || :|:|:|||
Db        245 RRKENKSRLNENKRVNVMLISIVVTFGACWLPLNIFNVIFDWYHEMLMSCHHDLVFVVCH 304

Qy        309 LLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSKGSLRL 368
              |:|| |||:||  ||||| ||:|::  |:  |    | |  |:: :||:||: |||||:|
Db        305 LIAMVSTCINPLFYGFLNKNFQKDLMMLIHHCWCGEPQESYENIAMSTMHTDESKGSLKL 364

Qy        369 S 369
              :
Db        365 A 365


RESULT 11
US-09-962-646-15
; Sequence 15, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION:
;  APPLICANT: GERALD, CHRISTOPHE P.G.
;  APPLICANT:  WEINSHANK, RICHARD L
;  APPLICANT:  WALKER, MARY W
;  APPLICANT:  BRANCHEK, THERESA
;  TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
;  TITLE OF INVENTION:  ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPT
;  FILE REFERENCE: 1795/46166BZA
;  CURRENT APPLICATION NUMBER: US/09/962,646
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 09/200,673
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: 08/566,096
;  PRIOR FILING DATE: 1995-12-01
;  PRIOR APPLICATION NUMBER: 08/349,025
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;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-962-646-15

  Query Match             43.8%;  Score 860.5;  DB 9;  Length 384;
  Best Local Similarity   44.9%;  Pred. No. 1.1e-69;
  Matches  167;  Conservative   77;  Mismatches  107;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||          |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| ||| |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPLTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|     |:   || || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |      |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| ||||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
              ||:   :::|:
Db        362 TSLK---QASPV 370


RESULT 12
US-09-771-956-2
; Sequence 2, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
;  APPLICANT:  Bennett, Michele
;  APPLICANT:  Brodbeck, Robbin
;  APPLICANT:  Krause, James
;  TITLE OF INVENTION:  Chimeric Neuropeptide Y Receptors
;  FILE REFERENCE:  N2000.001
;  CURRENT APPLICATION NUMBER: US/09/771,956
;  CURRENT FILING DATE:  2001-01-29
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-771-956-2

  Query Match             43.6%;  Score 856.5;  DB 9;  Length 384;
  Best Local Similarity   44.6%;  Pred. No. 2.6e-69;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||          |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| ||| |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|     |:   || || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |      |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| ||||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
              ||:   :::|:
Db        362 TSLK---QASPV 370


RESULT 13
US-09-393-696-23
; Sequence 23, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-393-696-23

  Query Match             43.6%;  Score 856.5;  DB 10;  Length 384;
  Best Local Similarity   44.6%;  Pred. No. 2.6e-69;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||          |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| ||||:|:|||||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|     |:   || || : :|    ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |      |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| ||||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
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Db        362 TSLK---QASPV 370


RESULT 14
US-10-410-648-4
; Sequence 4, Application US/10410648
; Publication No. US20040072847A1
; GENERAL INFORMATION:
;  APPLICANT: Bakthavatchalam, Rajagopal
;  APPLICANT:  Blum, Charles  A.
;  APPLICANT:  Brielmann, Harry L.
;  APPLICANT:  Darrow, James W.
;  APPLICANT:  De Lombaert, Stephane W.
;  APPLICANT:  Hutchinson, Alan W.
;  APPLICANT:  Tran, Jennifer W.
;  APPLICANT:  Zheng, Xiaozhang W.
;  APPLICANT:  Elliott, Richard  L.
;  APPLICANT:  Hammond, Marlys L.
;  TITLE OF INVENTION: SPIRO[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
;  TITLE OF INVENTION:  3H-SPIROISOBENZOFURAN-1,4'-PIPERIDINES
;  FILE REFERENCE: U 014539-7
;  CURRENT APPLICATION NUMBER: US/10/410,648
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: 10/013,846
;  PRIOR FILING DATE: 2001-12-11
;  PRIOR APPLICATION NUMBER: 60/254,990
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-410-648-4

  Query Match             43.6%;  Score 856.5;  DB 12;  Length 384;
  Best Local Similarity   44.6%;  Pred. No. 2.6e-69;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||            |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| |||:|:|||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|   |:   || || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |       |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| ||||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
              ||:   :::|:
Db        362 TSLK---QASPV 370


RESULT 15
US-10-013-846-4
; Sequence 4, Application US/10013846
; Publication No. US20030036652A1
; GENERAL INFORMATION:
;  APPLICANT: Bakthavatchalam, Rajagopal
;  APPLICANT:  Blum, Charles  A
;  APPLICANT:  Brielmann, Harry L
;  APPLICANT:  Darrow, James W
;  APPLICANT:  De Lombaert, Stephane
;  APPLICANT:  Hutchison, Alan
;  APPLICANT:  Tran, Jennifer
;  APPLICANT:  Zheng, Xiaozhang
;  APPLICANT:  Elliott, Richard L
;  APPLICANT:  Hammond, Marlys
;  TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
;  TITLE OF INVENTION:  3H-spiroisobenzofuran-1,4'-piperidines
;  FILE REFERENCE: N00.2001
;  CURRENT APPLICATION NUMBER: US/10/013,846
;  CURRENT FILING DATE:  2001-12-11
;  PRIOR APPLICATION NUMBER: US 60/254,990
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: homosapiens
US-10-013-846-4

  Query Match             43.6%;  Score 856.5;  DB 14;  Length 384;
  Best Local Similarity   44.6%;  Pred. No. 2.6e-69;
  Matches  166;  Conservative   77;  Mismatches  108;  Indels   21;  Gaps    5;

Qy         16 QGENRSKPLGTPYNFSE----------HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
              | || |       ||||            |   : ::  :  :|    ::|| ||| |:
Db          8 QVENHS----VHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

Qy         65 VTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
              : ::|||  ||||:|| ||:||| |: ::| | | |||:||:|:||| :||:: |:||:|
Db         64 IILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVS 123

Qy        125 VTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVF 184
              :|||| |||:|:|||||||| ||:|:   ||:|| :|||:|   |||||   :: :
Db        124 ITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDEP 183

Qy        185 HKNHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRLQRQ 244
              :|   |:   || || : :|   ||  ||| ||: ||  || || :|| :|| ||:|:
Db        184 FQN--VTLDAYKDKYVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRR 241

Qy        245 GRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAVLWLPLHVFNSLEDWHHEAIPICHGNLI 303
              :  |       |:   |::|::|: :|||||| |||| :||:: ||:|: |  |: ||:
Db        242 NNMMDKMRDNKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLL 301

Qy        304 FLVCHLLAMASTCVNPFIYGFLNTNFKKEIKALVLTCQQSAPLEESEHLPLSTVHTEVSK 363
              ||:||| || |||||| ||||| ||:::::     |   :  :: | : :||:||:|||
Db        302 FLLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFFNFCDFRSRDDDYETIAMSTMHTDVSK 361

Qy        364 GSLRLSGRSNPI 375
              ||:   :::|:
Db        362 TSLK---QASPV 370


Search completed: May 11, 2004, 13:05:05
Job time : 49 secs
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